Georeferenced database of genetic diversity
(GD)²
User Manual

Properties	
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I. Objectives

This database contains genetic and georeferenced passport data of different genetic units that are traditionally analyzed by geneticists and ecologists.
Genetic data include marker data (Microsatellites, Single nucletotide polymorphisms, PCR DNA fragments etc...) coming either from diploid or haploid tissue for wich genetic parameters have been calculated (allelic or nucleotide frequencies, diversity statistics).
Passport data include all other data than genetic, ranging from geographic coordinates to ecological or physiographic data of the location of the genetic units.
Genetic units are either single individuals or populations on which the genetic and passport data are recorded.

Specific objectives of the applications are :
- 1: Insert genetic and georeferenced data of natural populations
- 2: View geographic distribution of data
- 3: Export data to different format (CSV, GIS format, population genetic software format) for data analysis

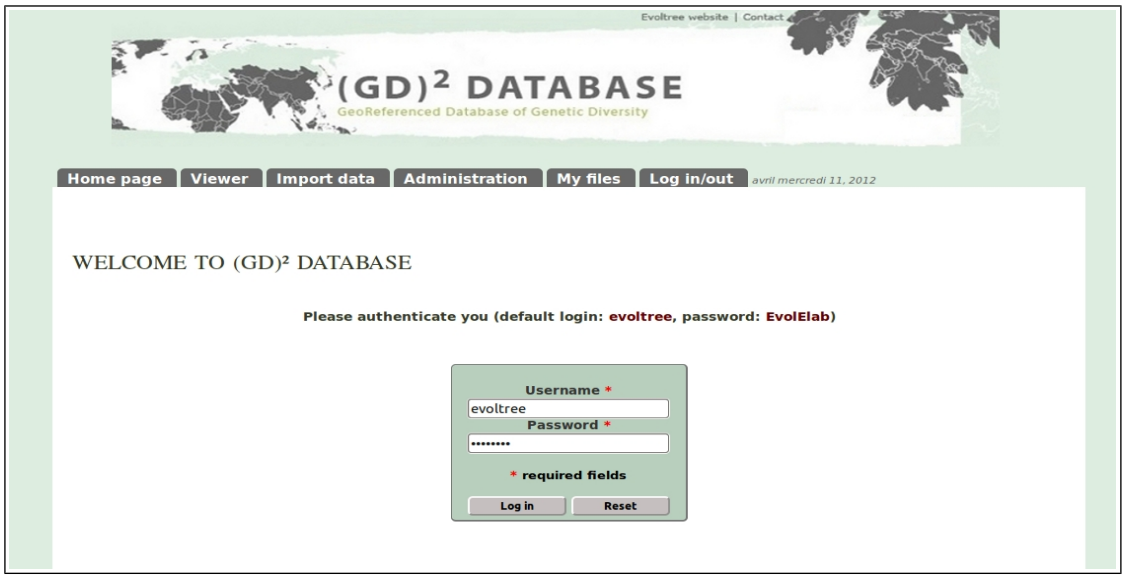
II. Organisation and technical informations

1. Technical informations

(GD)² is implemented in Ruby On Rails 2 and is optimized for Mozilla Firefox. Database is managed by PostgreSQL (version 8.4) and PostGIS. Maps are provided by Google MapsTM.

2. Organisation

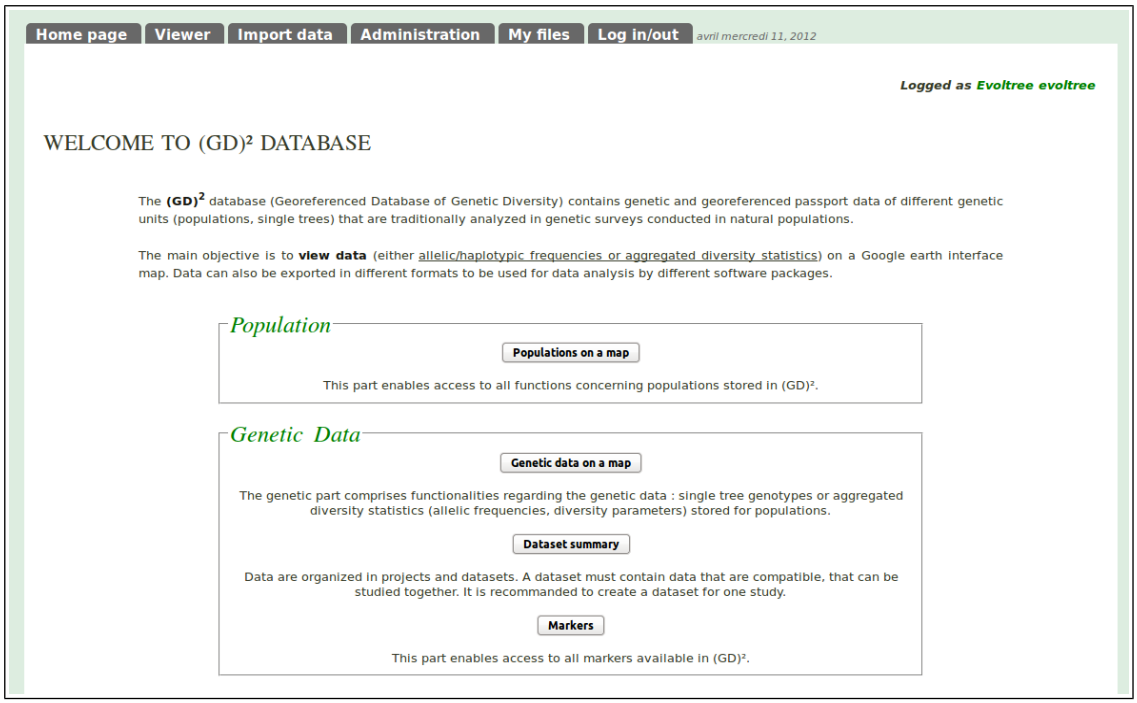
1) Login page



Authentication is necessary to access to (GD)². Login and password are provided by the administrator and are defined as follow:
- first letter of the first name in upper-case followed by the name (with the first letter in upper-case too)
- an example : for Mr John Doe, it's JDoe.

2) Home page and main parts of (GD)²

The home page allows access to the two main parts of the software. The menu on the top provides access to viewer, importation functionalities, data administration and to saved files.


Home page
Viewer
Import data
Administration
My files
Log in/out
avril mercredi 11, 2012
Logged as Evoltree evoltree
WELCOME TO (GD)² DATABASE
The (GD)² database (Georeferenced Database of Genetic Diversity) contains genetic and georeferenced passport data of different genetic units (populations, single trees) that are traditionally analyzed in genetic surveys conducted in natural populations.
The main objective is to view data (either allelic/haplotypic frequencies or aggregated diversity statistics) on a Google earth interface map. Data can also be exported in different formats to be used for data analysis by different software packages.
Population
Populations on a map
This part enables access to all functions concerning populations stored in (GD)².
Genetic Data
Genetic data on a map
The genetic part comprises functionalities regarding the genetic data : single tree genotypes or aggregated diversity statistics (allelic frequencies, diversity parameters) stored for populations.
Dataset summary
Data are organized in projects and datasets. A dataset must contain data that are compatible, that can be studied together. It is recommanded to create a dataset for one study.
Markers
This part enables access to all markers available in (GD)².

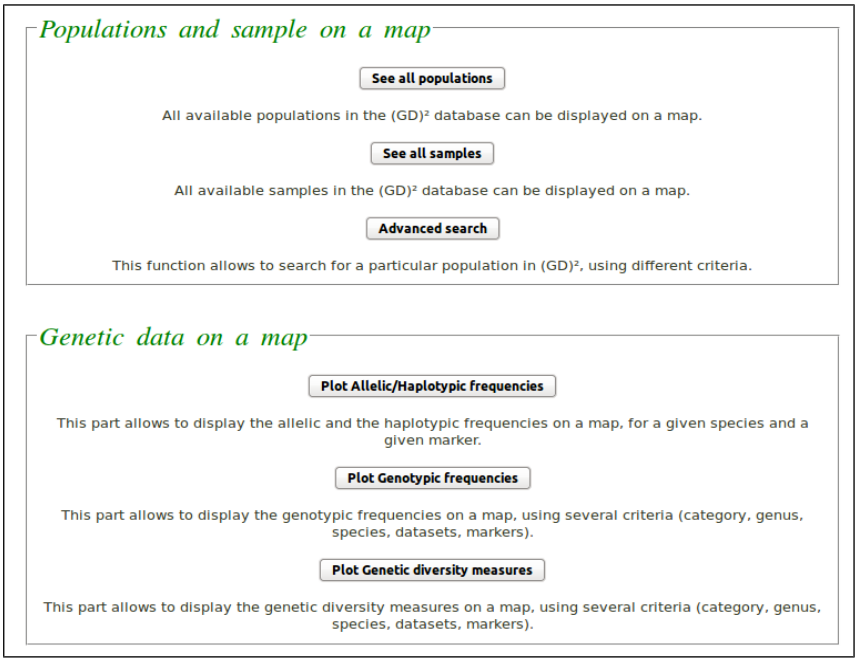
(a) "Population" part

This part enables access to all functions concerning populations stored in (GD)².

(b) "Genetic Data" part

The genetic part comprises functionalities regarding the genetic data : single tree genotypes or aggregated diversity statistics (allelic frequencies, diversity parameters) stored for populations, dataset summary and markers.

These two categories are also available using the "Viewer" menu.


Populations and sample on a map
See all populations
All available populations in the (GD)² database can be displayed on a map.
See all samples
All available samples in the (GD)² database can be displayed on a map.
Advanced search
This function allows to search for a particular population in (GD)², using different criteria.
Genetic data on a map
Plot Allelic/Haplotypic frequencies
This part allows to display the allelic and the haplotypic frequencies on a map, for a given species and a given marker.
Plot Genotypic frequencies
This part allows to display the genotypic frequencies on a map, using several criteria (category, genus, species, datasets, markers).
Plot Genetic diversity measures
This part allows to display the genetic diversity measures on a map, using several criteria (category, genus, species, datasets, markers).

II. Functionalities

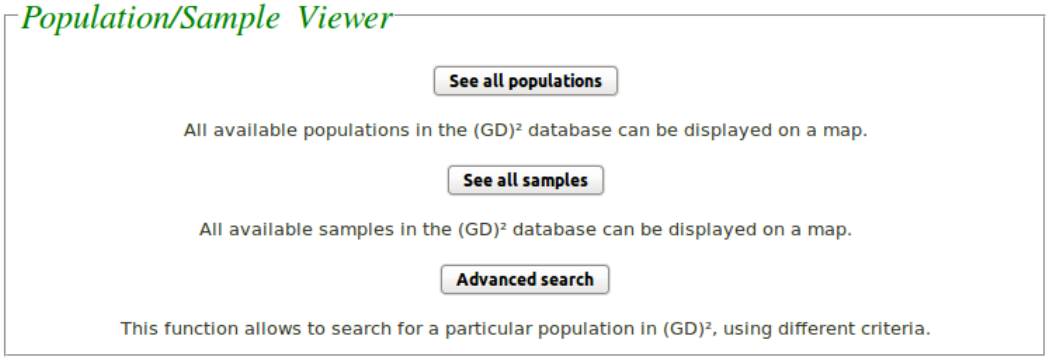
1. Viewer

Main function of (GD)², the Viewer permits to display different informations on a geographical map. This function is accessible from the menu or by clicking on “Population on map” button or on “Genetic data on map” button in the home page.

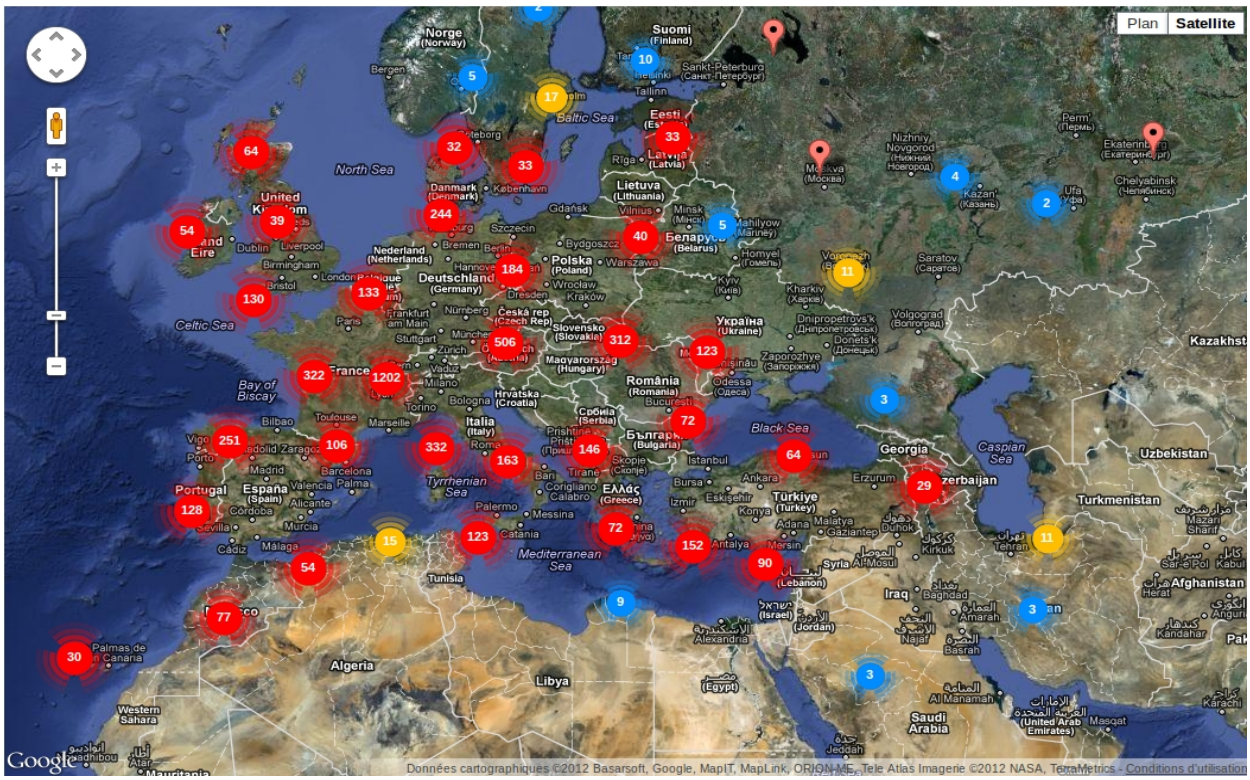
1) Populations and sample on a map

(a) See all populations

All available populations can be displayed on a map by clicking on “See all populations” button. Under the map, a list of these populations, sorted by country, is displayed with their main characteristics. By clicking on population's name in the list, you will focus on this population on the map.

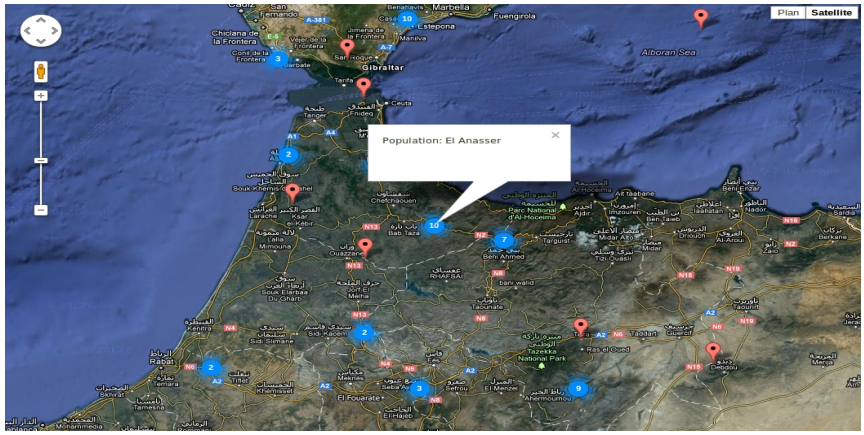

Population/Sample Viewer
See all populations
All available populations in the (GD)² database can be displayed on a map.
See all samples
All available samples in the (GD)² database can be displayed on a map.
Advanced search
This function allows to search for a particular population in (GD)², using different criteria.

Map obtained with function “See all populations”



Morocco

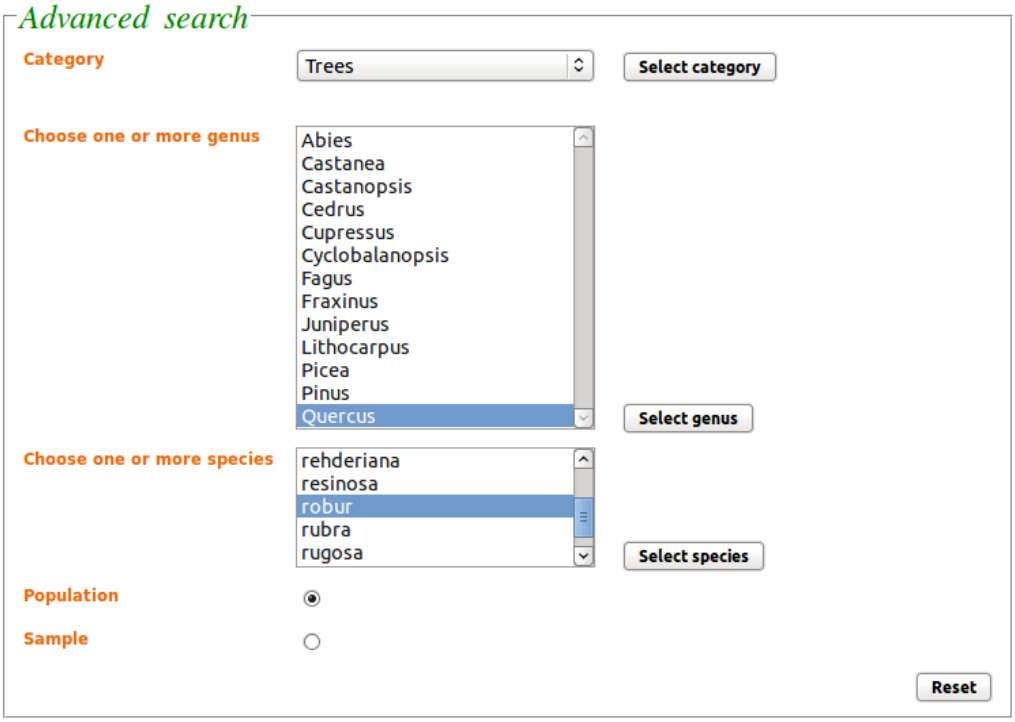
Population	Species	latitude	longitude	Altitude	Country	Number of individuals
El Anasser	canariensis	-5.0	35.03	1260	Morocco	2
Pmo	pinaster	-5.1	33.87		Morocco	117
Bucci_2007_33870000_-4030000_NA	pinaster	-4.03	33.87	0	Morocco	0



(b) Advanced search

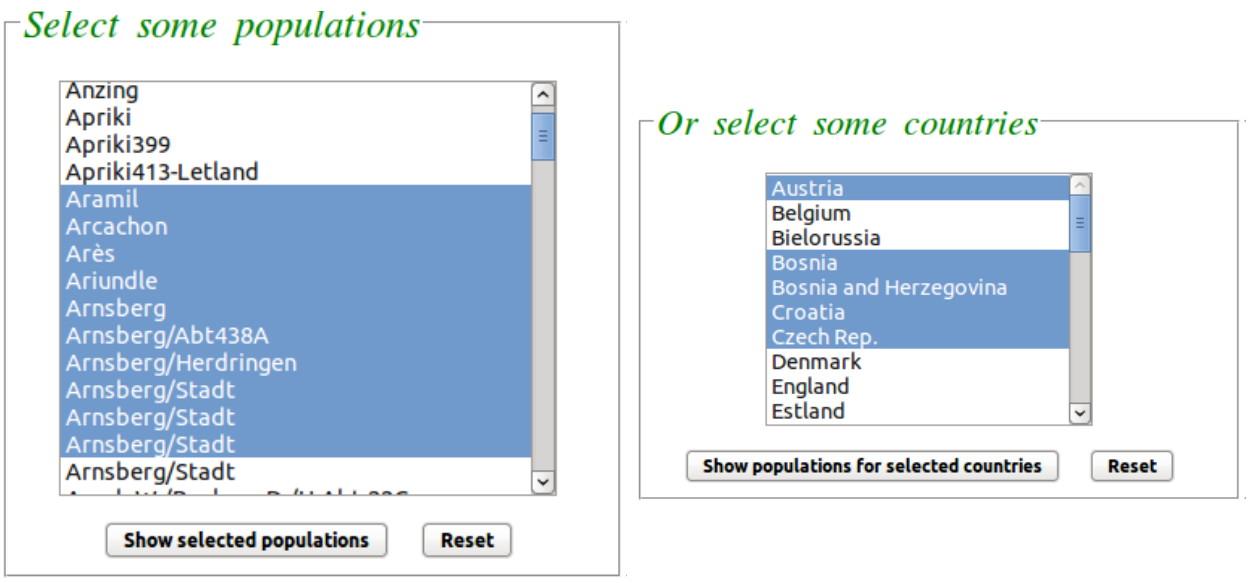
This function allows to search for a particular population. To do so, the following items must be selected :

- the category (fungi, insects or trees)
- the genus (one or more)
- the species (one or more)
- if you want a population or a sample (check boxes “population” or “sample”)
- Click on the “Select species” button to display results.



From this first selection, two lists are obtained. They permit :

- to select some populations to display on a map.
- to select countries so that all populations located in the country can be displayed.



Under the map, like the "See all populations" function, a list of the populations is available, sorted by country. Two links are available: "View individuals", which allows to display individuals contained in each populations , and "View individual data", which allows the display of available genotyping data for a given population.

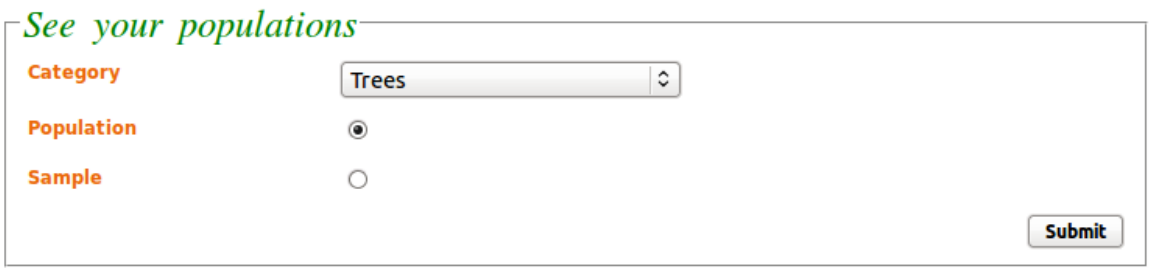
Austria

Population	Species	Origin	longitude	latitude	Altitude	Country	Number of individuals		
Stamser_89	robur		11.0	47.5	660	Austria	76	View individuals	View individual data
KG Kössen	robur	autochthonous	12.4	47.68	600	Austria	6	View individuals	View individual data
KG Ebbs/Sportplatz	robur	autochthonous	12.24	47.65	470	Austria	2	View individuals	View individual data
Kaisertal /Kufstein	robur	autochthonous	12.21	47.61	650	Austria	3	View individuals	View individual data
KG Thiersee/Pirchmoos	robur	autochthonous	12.05	47.61	770	Austria	2	View individuals	View individual data
KG Kirchdorf	robur	autochthonous	12.45	47.56	690	Austria	5	View individuals	View individual data

(c) See your populations

From this part of the application you can also visualized the populations that you have inserted. To do so, the following items must be selected :

- the category (fungi, insects or trees)
- if you want a population or a sample (check boxes "population" or "sample")



NB: The display for populations can change according the level zoom. When the number of populations to display is large, one icon actually represents several populations.. The information window who displays by clicking on the icon will contain a list with the eight first populations and the complete number of populations left. All the populations can be displayed if you further focus on the icon.

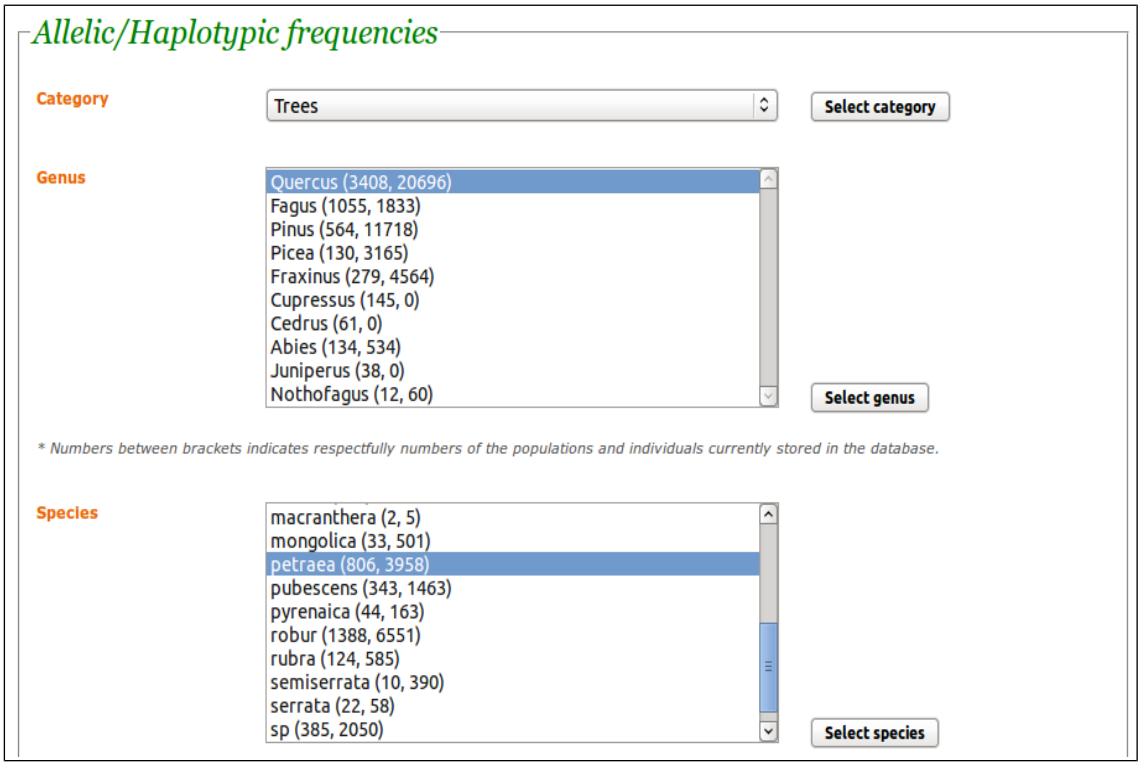
2) Genetic data on map

This function allows to display the allelic frequencies, the haplotypic frequencies, the genotypic frequencies or the different diversity indices on a geographical map.

(a) Plot Allelic/Haplotypic frequencies

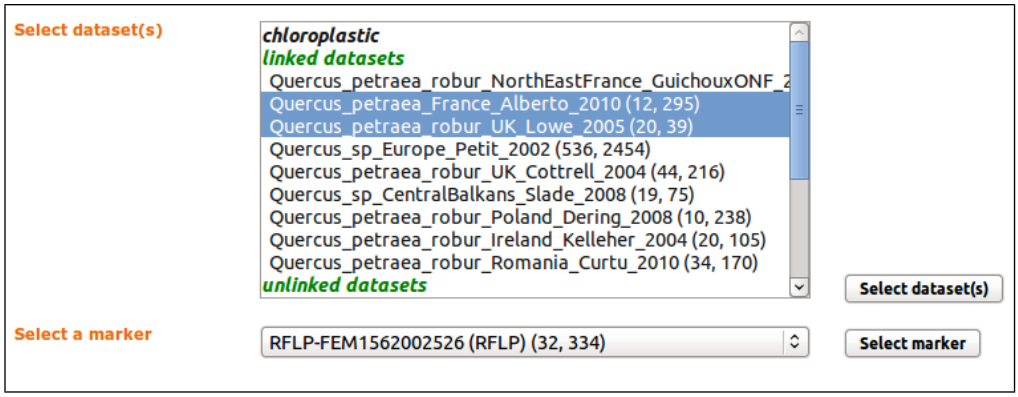
The display of allelic (or haplotypic) frequencies is realised for a given species and a given marker. So, must be selected :

- a category
- one or more genus
- one or more species

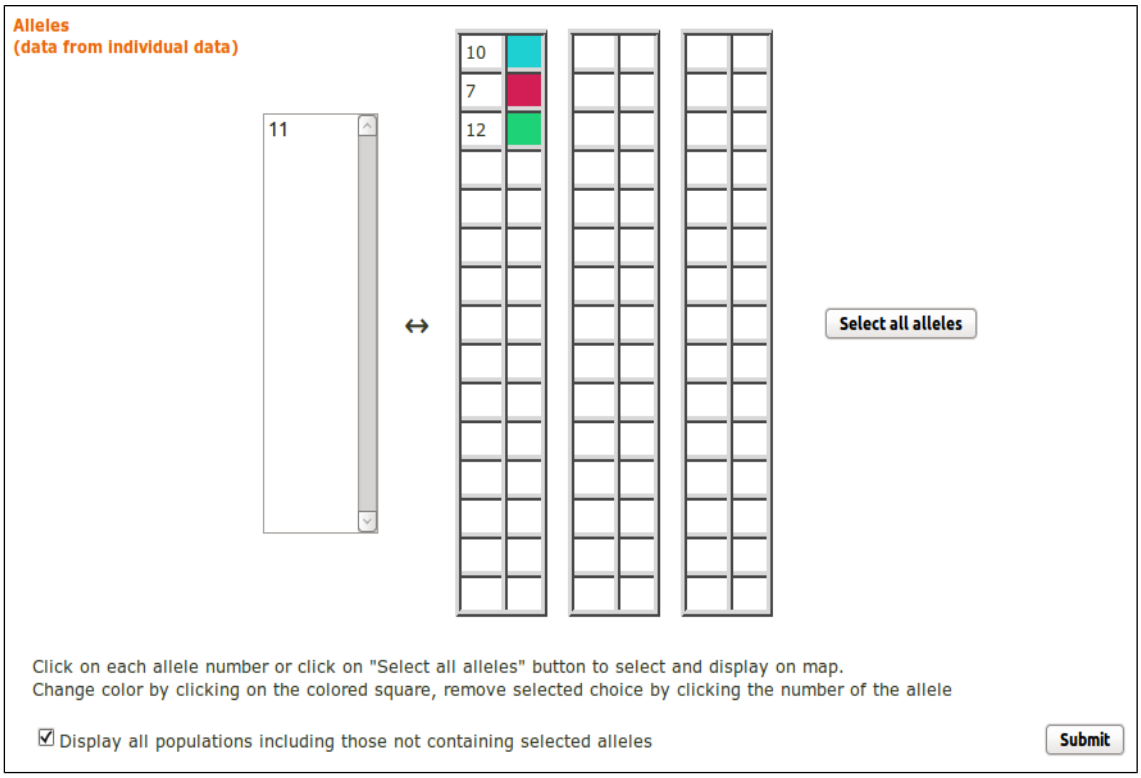


From this selection, then must be selected :

- one or more dataset : datasets are organized into two sections, corresponding to the different compartment **chloroplastic** and **nuclear.** Datasets in these two sections can be **linked** or **unlinked** (two datasets are linked when the study uses the same names and descriptions of markers
- the marker



Then just select the desired alleles (or haplotypes) for the display. Click on each allele number or click on "Select all alleles" button to select and display on map. Change color by clicking on the colored square, remove selected choice by clicking the number of the allele. You can also display all populations including those not containing selected alleles.


Alleles
(data from individual data)
11
10
7
12
Select all alleles
Click on each allele number or click on "Select all alleles" button to select and display on map.
Change color by clicking on the colored square, remove selected choice by clicking the number of the allele
Display all populations including those not containing selected alleles
Submit

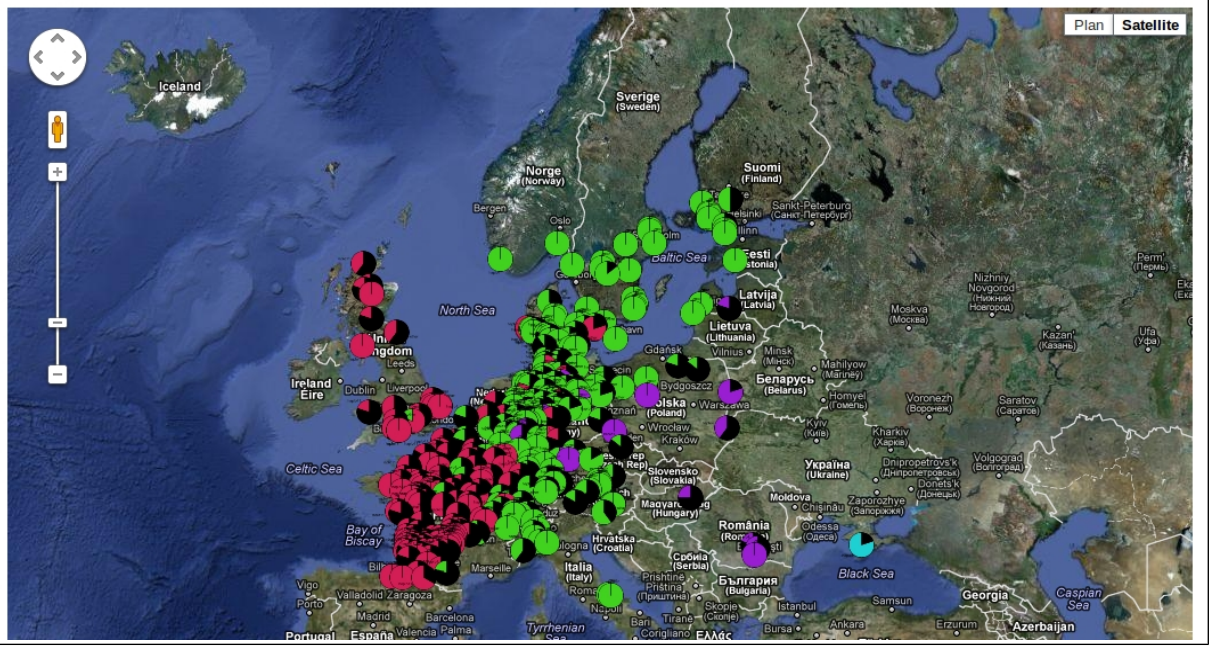
On the map, frequencies are represented by pie charts . The list of the populations is available as usual, with the possibility to download the pie chart for each population. Click on population name in the list to visualize it on the map (see below).

RESULTS FOR ALLELIC/HAPLOTYPIC FREQUENCIES

Marker name : RFLP-FEM1562002526

Alleles : haplo1 => #40d21e | haplo11 => #d21e55 | haplo8 => #1ed0d2 | haplo4 => #991ed2 |

Fullscreen



Populations in Dataset(s)

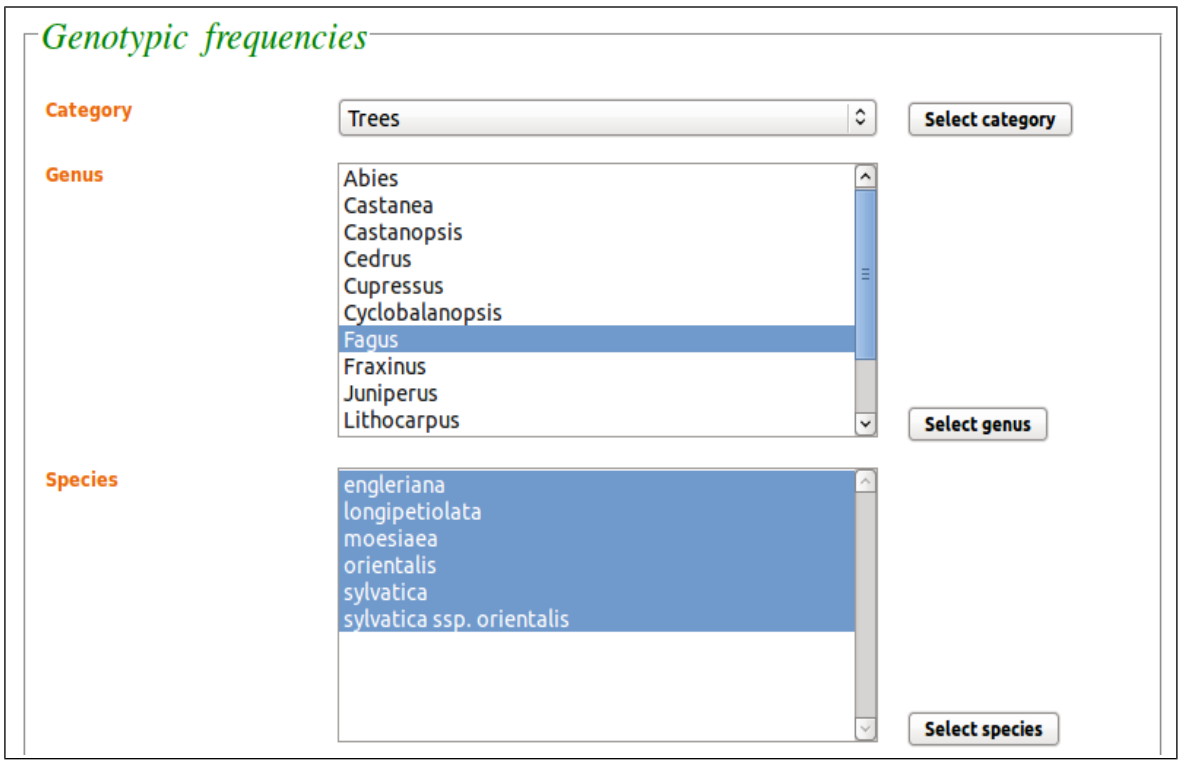
Population name	Species	Download the graphic
694	Quercus robur	Load
748	Quercus robur	Load
841	Quercus robur	Load
Abzac	Quercus robur	Load
Aisenay	Quercus robur	Load
Aistersheim	Quercus robur	Load
Algsjø-Finland	Quercus robur	Load
Altenplathow/Altenpl.	Quercus robur	Load
Anröchte/Abt.32A,B,C	Quercus robur	Load
Apriki	Quercus robur	Load
Apriki399	Quercus robur	Load
Apriki413-Letland	Quercus robur	Load
Arcachon	Quercus robur	Load
Arès	Quercus robur	Load
Arnsberg	Quercus robur	Load
Arnsberg/Abt438A	Quercus robur	Load

NB: if all alleles (or haplotypes) are not selected in the form, in the pie chart, the black parts will represent the proportion of non selected alleles.

(b) Plot genotypic frequencies

The display of genotypic frequencies is realised for a given marker and genotype(s). So, must be selected :

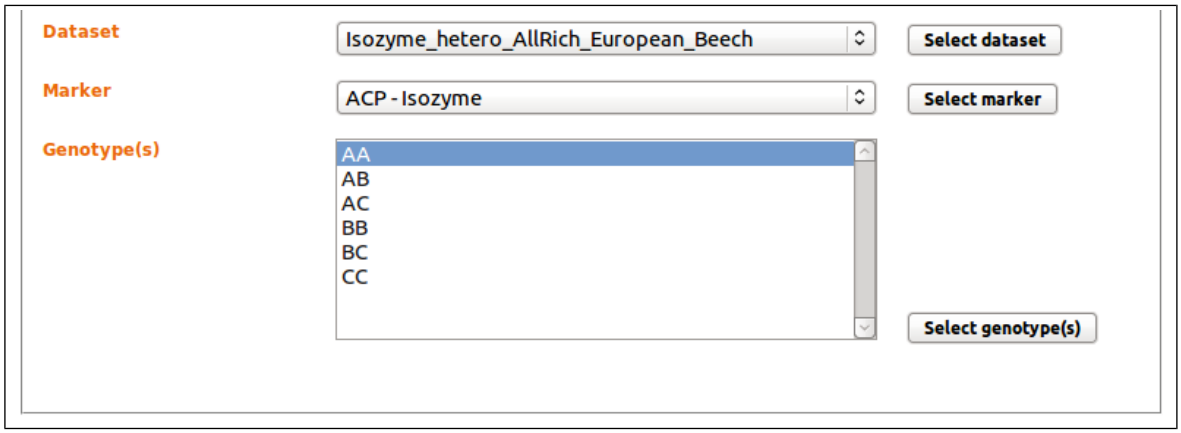
- a category
- one or more genus
- one or more species



From this selection, then must be selected :

- one dataset
- a marker

Then just select the desired genotype(s) for the display.

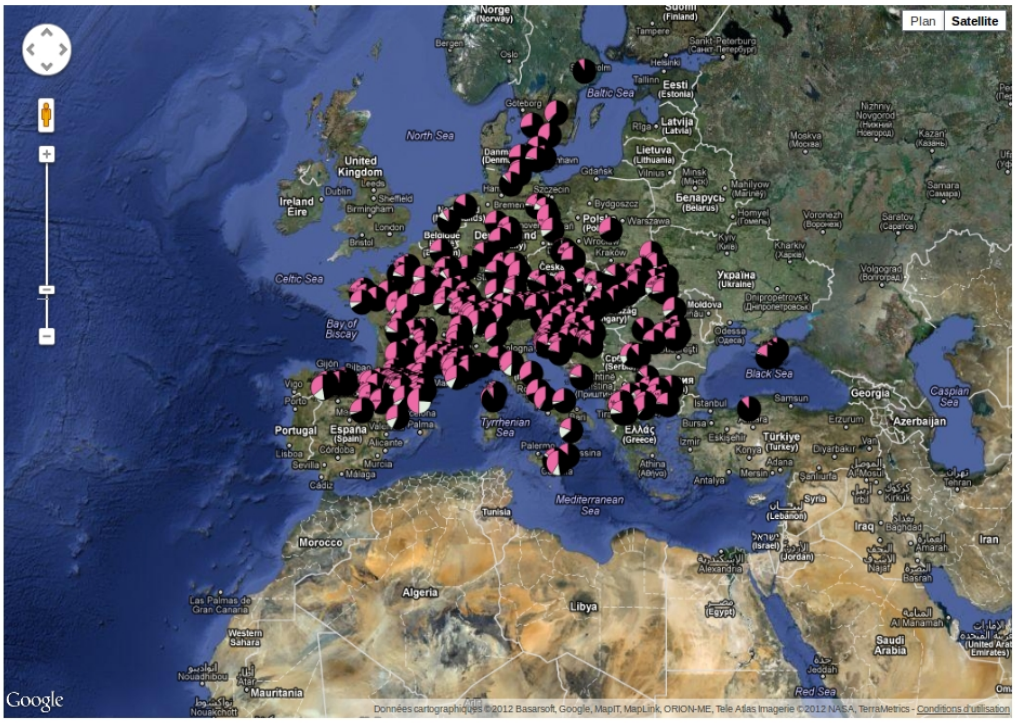


On the map, frequencies are represented by pie charts . The list of the populations is available as usual, with the possibility to download the pie chart for each population. Click on population name in the list to visualize it on the map (see below).

RESULTS FOR GENOTYPIC FREQUENCIES

Marker name : ACP

Fullscreen


Plan
Satellite
Google
Données cartographiques ©2012 Basarsoft, Google, MapIT, MapLink, ORION-ME, Tele Atlas Imagerie ©2012 NASA, TerraMetrics - Conditions d'utilisation

Dataset documentation : Isozyme_hetero_AllRich_European_Beech

(c) Plot genetic diversity measures

Populations in Dataset(s)

Population name	Species	Download the graphic
Abetone_1_210_34	Fagus sylvatica	Load
Abetone_2_211_34	Fagus sylvatica	Load
Abetone_3_212_34	Fagus sylvatica	Load
Abruzzes_205_32	Fagus sylvatica	Load
Achenkirch_335_53	Fagus sylvatica	Load
Aigoual_31_16	Fagus sylvatica	Load
Akulla_272_29	Fagus sylvatica	Load
Alba Iula_301_40	Fagus sylvatica	Load
Albères_61_5	Fagus sylvatica	Load
Altenburg_255_50	Fagus sylvatica	Load
Altengsbach_248_49	Fagus sylvatica	Load
Altube_60_13	Fagus sylvatica	Load
Amorbach_324_55	Fagus sylvatica	Load
Anie_40_11	Fagus sylvatica	Load
Anloo_81_56	Fagus sylvatica	Load
Apata_376_41	Fagus sylvatica	Load
Aralar_57_13	Fagus sylvatica	Load
Arbailles_384_12	Fagus sylvatica	Load
Arguenos_38_7	Fagus sylvatica	Load
Aspin_288_9	Fagus sylvatica	Load

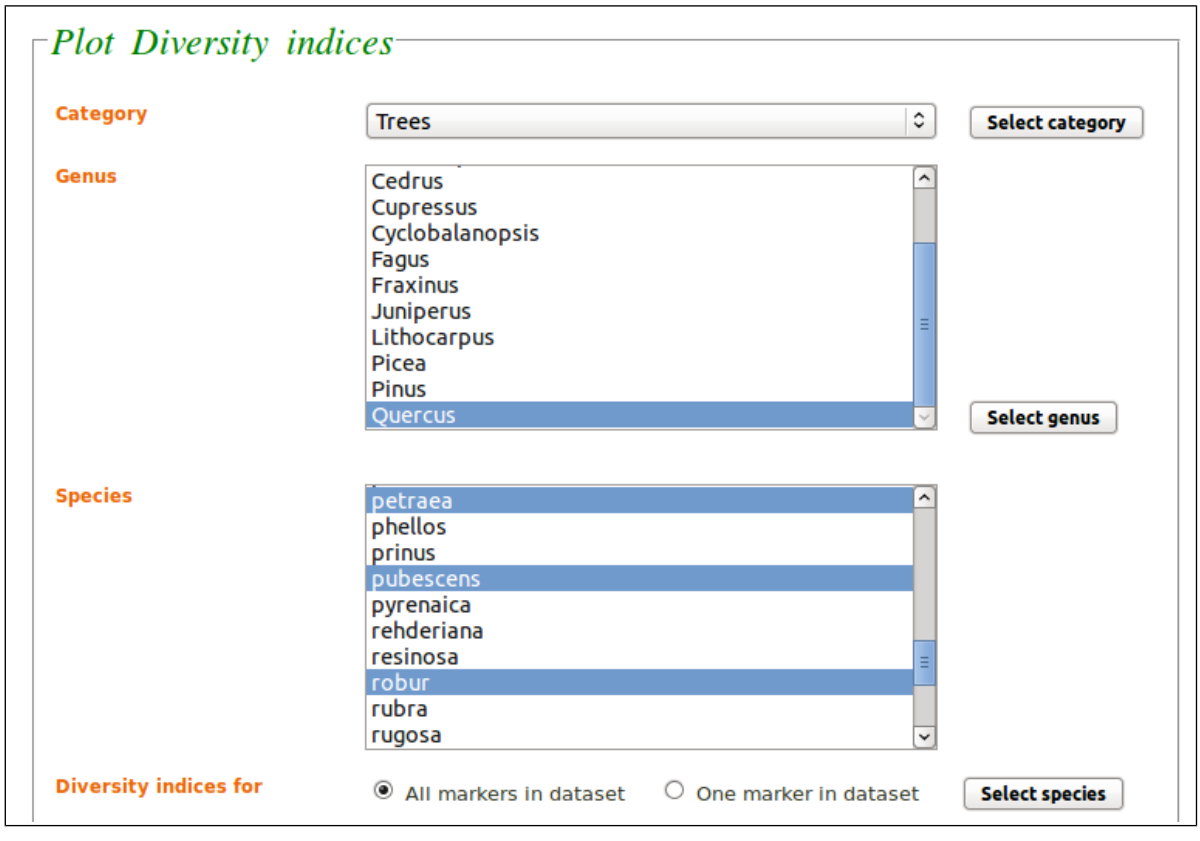
The display of genetic diversity measures is realised for a given species, a given marker and a given diversity indice.

Available diversity indices in (GD)² are :

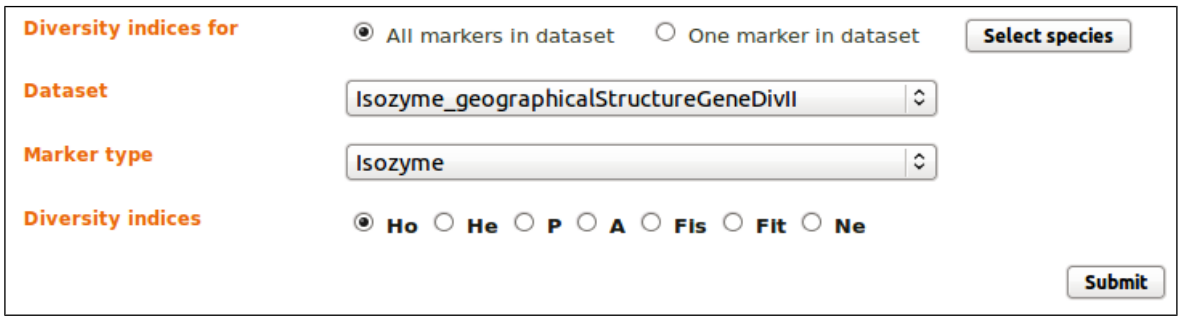
- Ho (Observed heterozygosity)
- He (Expect heterozygosity)
- P (Polymorphism rate)
- A (Allelic diversity)
- Fis, Fit (Inbreeding coefficients)

Thus, select :

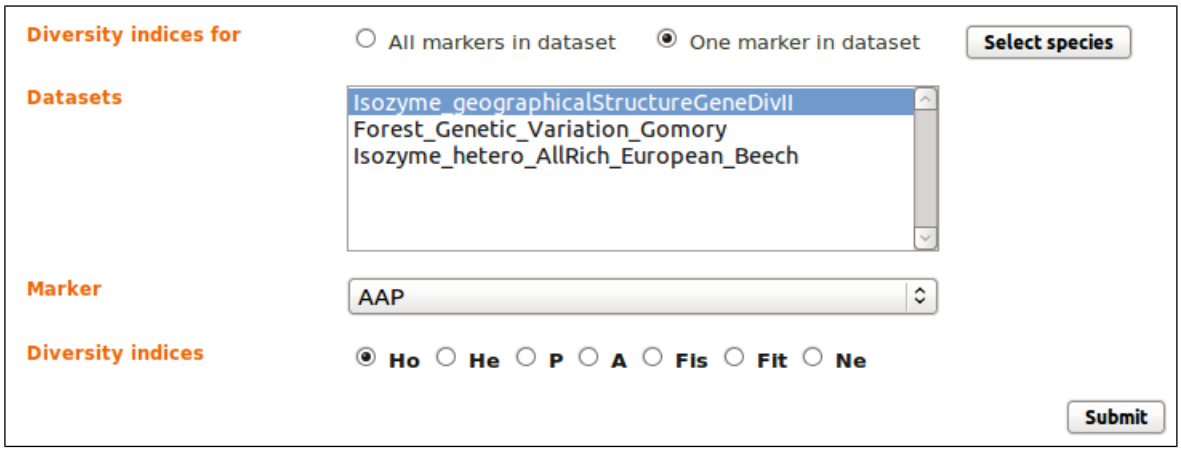
- the category
- the genus
- the species
- check one option for the diversity indices :
  - "Diversity indices for all markers in dataset" for indices calculated on a set of markers
  - "Diversity indices for one marker in dataset" for indices calculated for one marker



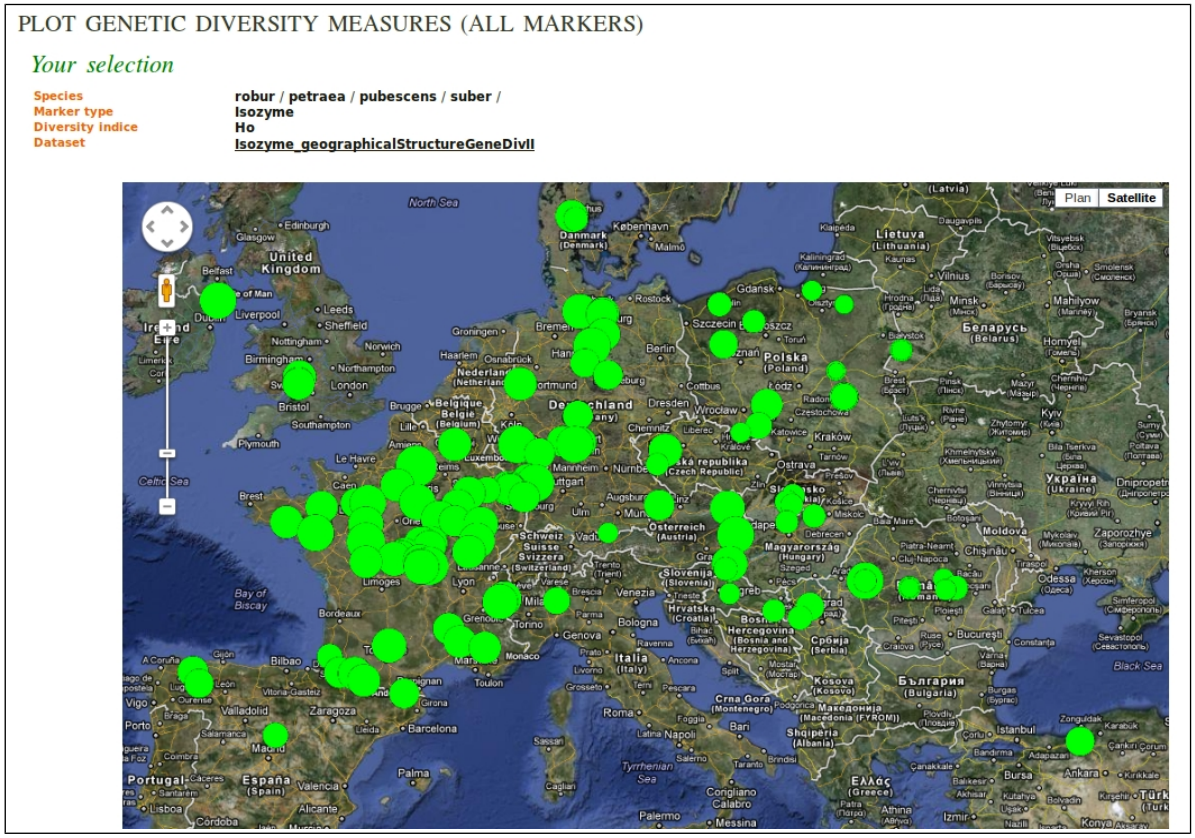
Depending the checked option, it's possible to choose a type of marker (first option)



or a marker (second option) for given dataset, and the index that will be displayed (check boxes).



We will obtain a map with circles that picturing the populations. Their diameter is proportional to the index's value.



The list of the populations is available as usual, with value of diversity indice selected, sorted by country. Click on population name in the list to visualize it on the map (see below).

Austria

Population	Species	Country	Ho
Stamser_89	robur	Austria	0.381269
Klostermarienberg_38	petraea	Austria	0.339454
Hainback_62	petraea	Austria	0.317122

Bosnia Herzegovina

Population	Species	Country	Ho
Arpatdteto_135	petraea	Bosnia Herzegovina	0.341402

Croatia

Population	Species	Country	Ho
Jasenovaca_83	robur	Croatia	0.265803

Czech Rep.

Population	Species	Country	Ho
Chudenice_116	robur	Czech Rep.	0.212072
Doubrava_117	petraea	Czech Rep.	0.255853

3) Markers

To view available markers in (GD)², the button “markers” on the home page and in the “Viewer” menu take to a menu where it is possible to :

- display all available markers
- do an advanced search

Show markers
View all markers
Display all available markers in (GD)² database.
Advanced search
This function allows to search for a particular markers in (GD)², using different criteria.

(a) All markers

All available markers are listed, sorted by marker type.

ALL MARKERS

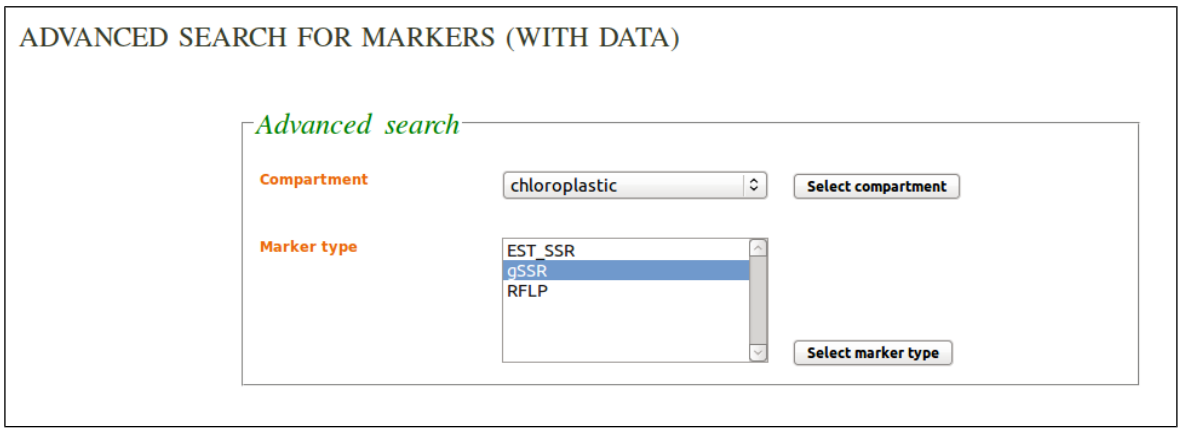
Marker type : gSSR

Marker name	Marker type	Compartment	Measure type	Sequence (SSR)	Reference	Remarks
CPM_haplotypes_11seq	gSSR	chloroplastic	haplotypic		NULL	11 microsatellites: 3655,1520,4110,8730,3025,9400,7195,2610,1100,6375,7995,1250
P 7195	gSSR	chloroplastic	allelic			
P 30249	gSSR	chloroplastic	allelic			
P 30141	gSSR	chloroplastic	allelic			

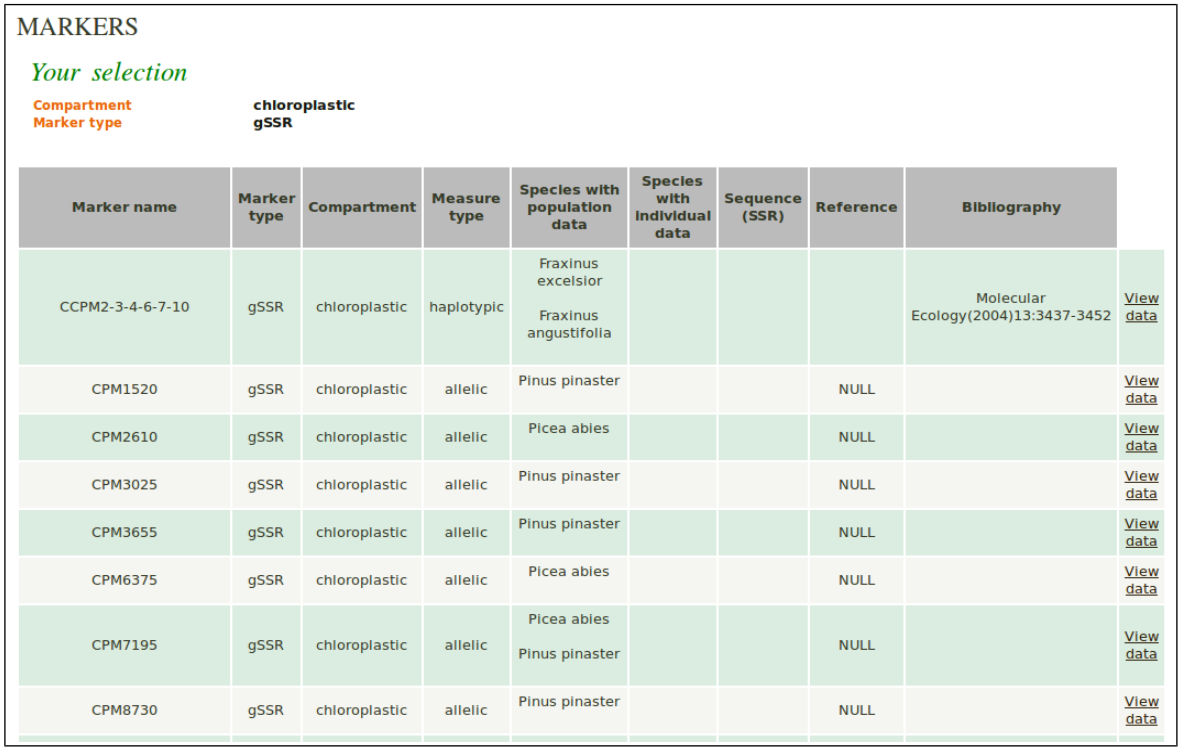
(b) Advanced search

To look for a marker is possible by selecting :

- the compartment (nuclear, cytoplasmic, mitochondrial,chloroplastic)
- the marker type (cpSSR, EST_SSR, RFLP, Isozyme)



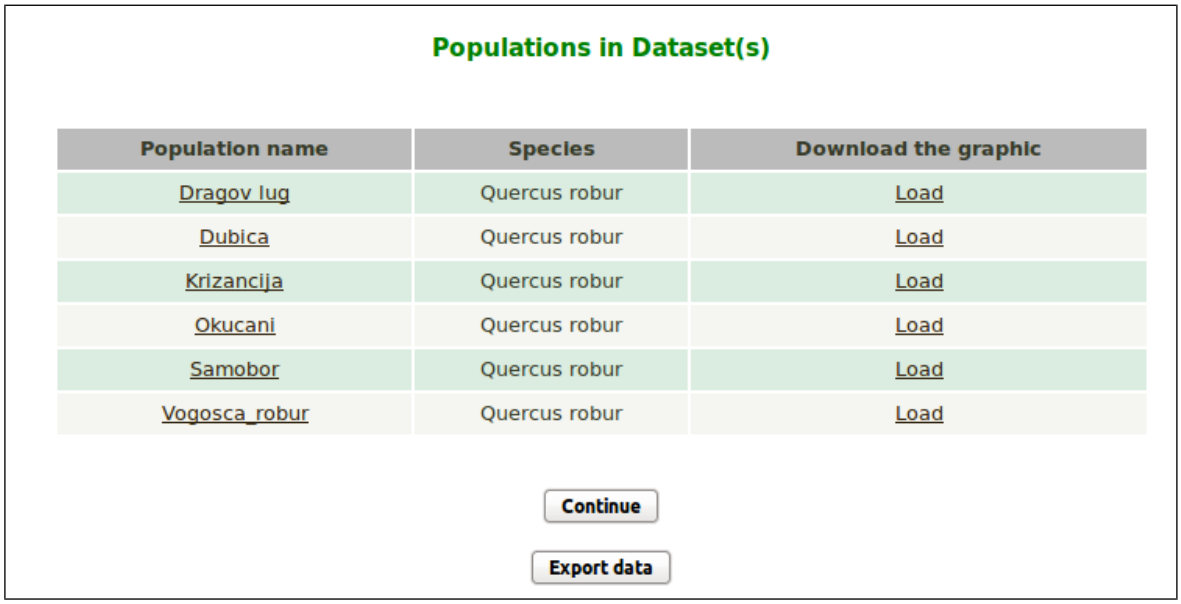
- the result is displayed in a list, and for each line, a link (View data) allows to localize all populations having data for the marker



Marker name	Marker type	Compartment	Measure type	Species with population data	Species with individual data	Sequence (SSR)	Reference	Bibliography	
CCPM2-3-4-6-7-10	gSSR	chloroplastic	haplotypic	Fraxinus excelsior Fraxinus angustifolia				Molecular Ecology(2004)13:3437-3452	View data
CPM1520	gSSR	chloroplastic	allelic	Pinus pinaster			NULL		View data
CPM2610	gSSR	chloroplastic	allelic	Picea abies			NULL		View data
CPM3025	gSSR	chloroplastic	allelic	Pinus pinaster			NULL		View data
CPM3655	gSSR	chloroplastic	allelic	Pinus pinaster			NULL		View data
CPM6375	gSSR	chloroplastic	allelic	Picea abies			NULL		View data
CPM7195	gSSR	chloroplastic	allelic	Picea abies Pinus pinaster			NULL		View data
CPM8730	gSSR	chloroplastic	allelic	Pinus pinaster			NULL		View data

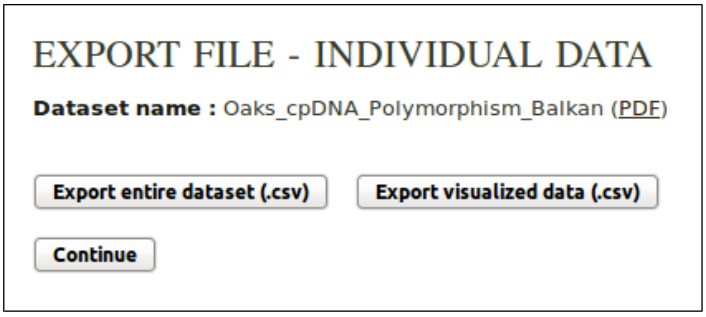
2. Exportation

Exportation is actually available for individual data, on allelic and (or) haplotypic frequencies. Exportation is accessible from the “Viewer”, when the geographical map is displayed with the frequencies distribution. “Export data” button is located under the “continue” button.

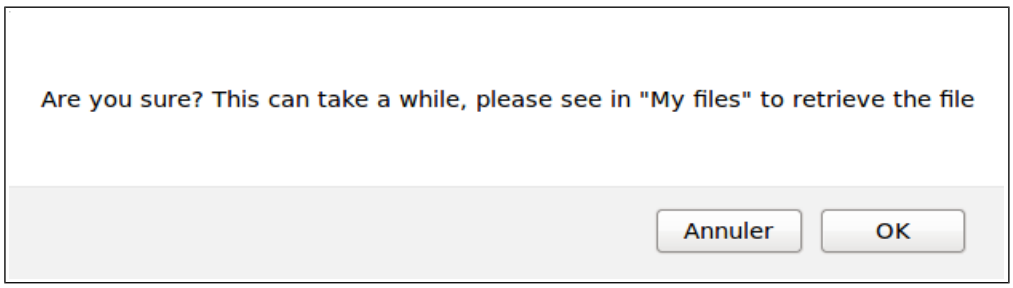


By clicking on it, there is two possibilities :

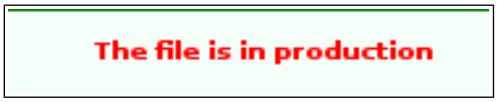
- export all data of the dataset
- export the previously displayed data



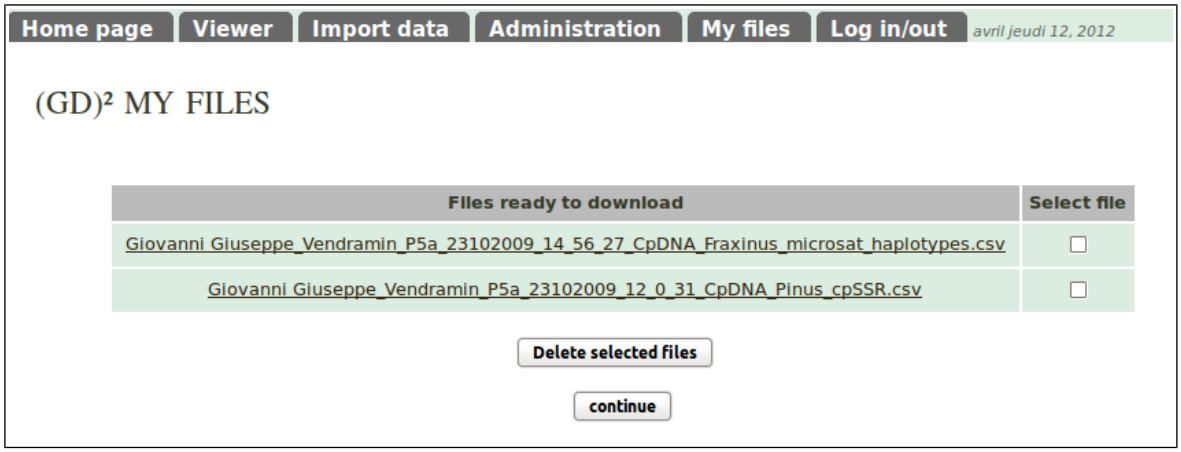
The exportation's format is in CSV.
By clicking on the chosen option, the exportation process is launched.



It's confirmed by a message on the top of the window

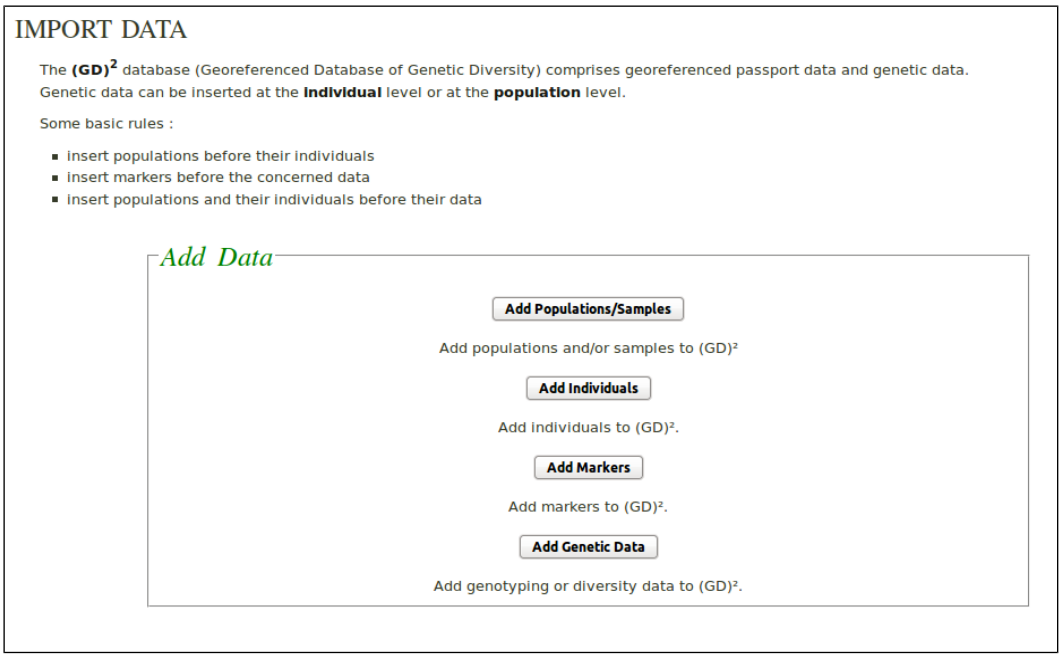


The file is then available in “My files” section of the web application. It can be downloaded or deleted.



3. Importation

The **(GD)^2** database (Georeferenced Database of Genetic Diversity) comprises georeferenced passport data and genetic data.
Genetic data can be inserted at the **individual** level or at the **population** level. For example, if you have already allelic frequencies and diversity statistics available, they can be inserted and will refer to the population level. If you have single tree genotypic data, they can be inserted at the individual level.
The importation function is accessible from the menu by clicking on “Import data”.

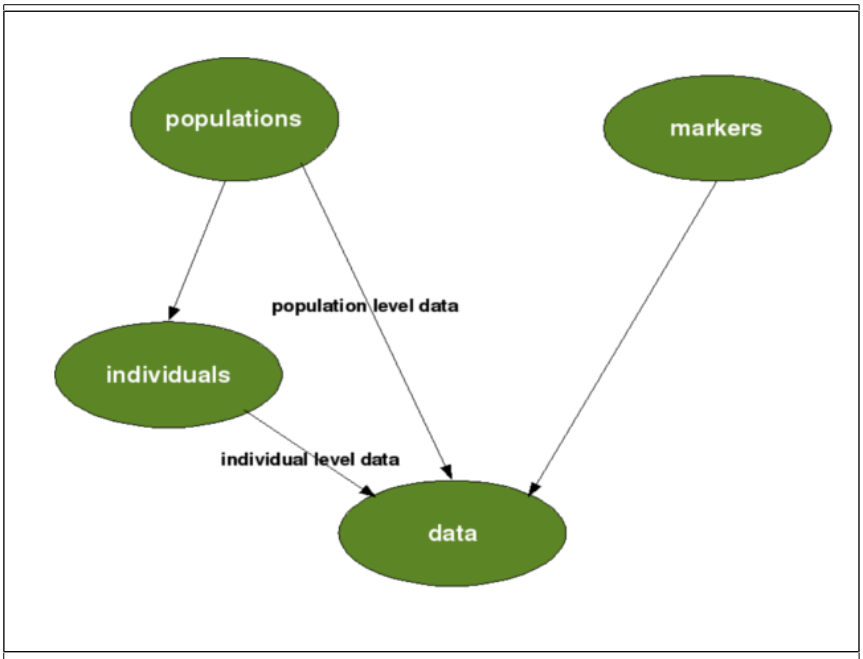

IMPORT DATA
The (GD)² database (Georeferenced Database of Genetic Diversity) comprises georeferenced passport data and genetic data.
Genetic data can be inserted at the individual level or at the population level.
Some basic rules :
insert populations before their individuals
insert markers before the concerned data
insert populations and their individuals before their data
Add Data
Add Populations/Samples
Add populations and/or samples to (GD)²
Add Individuals
Add individuals to (GD)².
Add Markers
Add markers to (GD)².
Add Genetic Data
Add genotyping or diversity data to (GD)².

The importation concerns the following items :

- populations/samples
- individuals
- markers
- genetic data

Some basic rules before inserting new data :

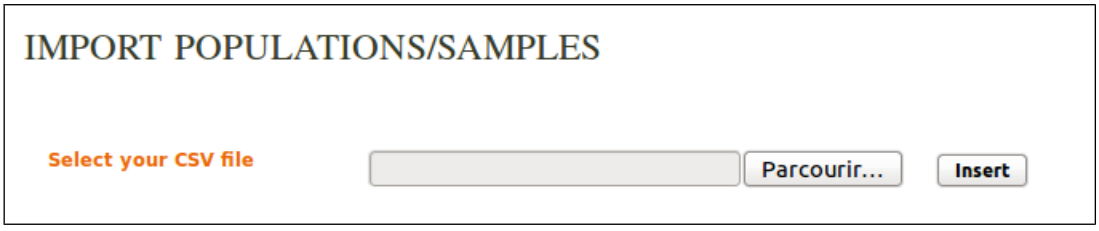
- insert populations before their individuals
- insert markers before the concerned data
- insert populations and their individuals before their data



All items upstream the arrows must be inserted before the items downstream the arrows

1) Import populations/samples

By clicking on “Add Populations/Samples”, we access to a simple form : just select the csv file and click on “insert” to upload the populations.



The csv file is presented below:

File format informations

First line : precise « population » or « sample »

File format : csv (delimiter is ,)

population									
population	species	long	lat	alt	country	laboratory	origin	stand	stand_name
Ficuzza_P6-0036	pubescens	13.36	37.86	1000	Italy	P6a	autochthonous	Forest	Ficuzza
Case Pintoria_P6-0051	pubescens	14.17	37.86	550	Italy	P6a	autochthonous	Forest	Case Pintoria
Pomieri Hotel_E	petraea	14.05	37.87		Italy	P1			Pomieri Hotel
Diga canna_E	petraea	14.07	37.87		Italy	P1			Diga canna
Castaño del Robledo_P10-090	sp	-6.72	37.89	375	Spain	P10	autochthonous	Forest	Castaño del Robledo
Godrano_P6-0038	pubescens	13.43	37.90	698	Italy	P6a	autochthonous	Forest	Godrano

Mandatory columns

- Population or sample name
- species
- long (longitude)
- lat (latitude)
- alt (altitude)
- country
- laboratory (Evoltree code)
- origin
- stand

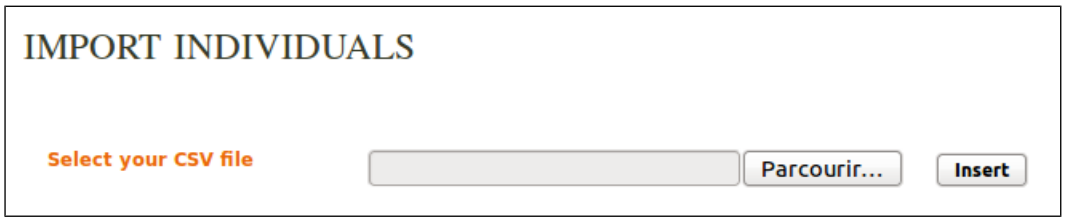
Facultative columns

- stand_name (forest name)
- region
- collect_date
- collector_name
- collect_method
- source
- stand_long
- stand_lat
- remarks

Respect the title of the columns (case and spelling). Latitudes and longitudes are in decimal degrees. Try to have as much as possible different names for your populations.

2) Import individuals

By clicking on “Add individuals”, we access to a simple form : just select the csv file and click on “insert” to upload individuals.



Individuals are inserted in the database **AFTER** their population. The csv file format is described below :

It is important that the population name in this file are the same that in the previous file : in other words, check that the file for populations and the file for individuals, contains the same population names.

File format informations

First line : precise « population » or « sample »

File format : csv (delimiter is ,)

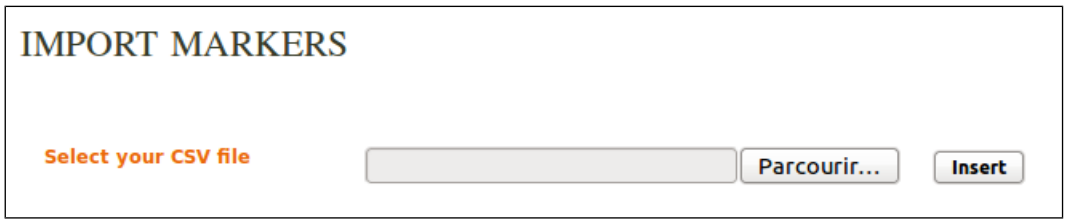
population		
name	population	species
mt-11	FDMonTravail	robur
mt-12	FDMonTravail	robur
mt-23	FDMonTravail	robur
mt-42	FDMonTravail	robur
mt-45	FDMonTravail	robur
mt-51	FDMonTravail	robur

Mandatory columns
- name
- population or sample
- species

Facultative columns
- lat (latitude)
- long (longitude)
- -

3) Import markers

By clicking on “Add markers”, we access to a simple form : just select the csv file and click on “insert” to upload markers.



Marker's types available in (GD)² are the following :

- EST_SSR (nuclear, chloroplastic, mitochondrial)
- gSSR (nuclear, chloroplastic)
- cpSSR (chloroplastic)
- RFLP (nuclear, chloroplastic, mitochondrial)
- SNP (nuclear)
- Isozyme (cytoplasmic)
- RAPD (nuclear)

File format informations

File format : csv (delimiter is ,)

name	type	measure_type	allele_type	compartment	biblio
marker1	EST_SSR	allelic		chloroplast	refXXX.pdf
marker2	SNP	allelic	codominant	nuclear	refX2X.pdf
marker3	RFLP	haplotype		chloroplast	refYXX.pdf

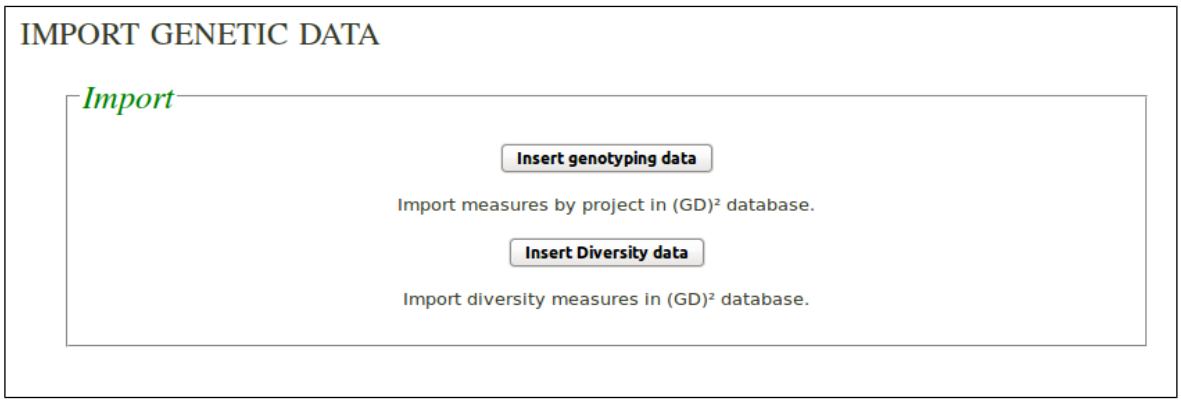
Mandatory columns
- name
- type
- measure_type
- compartment

Facultative columns
- sequence
- allele_type
- biblio
- -

The allele types can be “dominant” or “codominant”. For the genetic measures, there are two possible options: “allelic” or “haplotypic”. A column titled “reference” can be added for isozymes. The column “biblio” can be added providing a pdf file of the publication where the data were analysed for the first time.

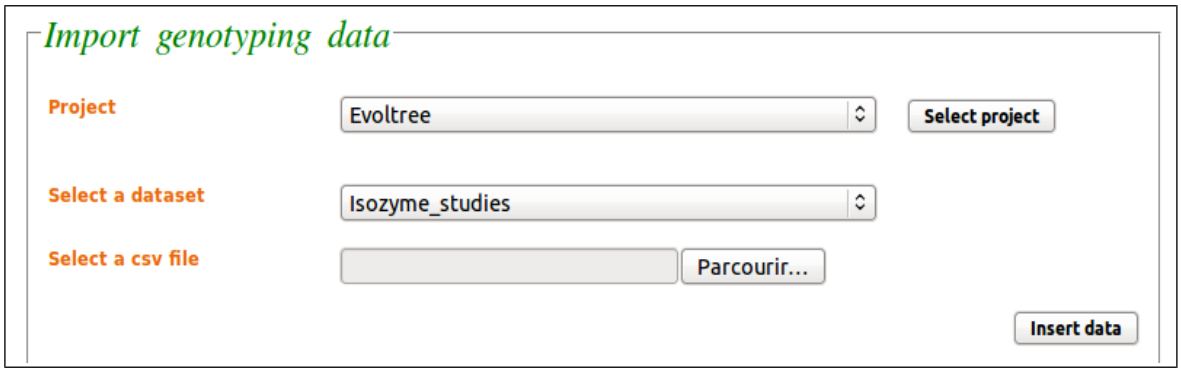
4) Import genetic data (measures)

To import genetic data, click on “Add genetic data”. You can import measures by project or import diversity measures in (GD)² database.



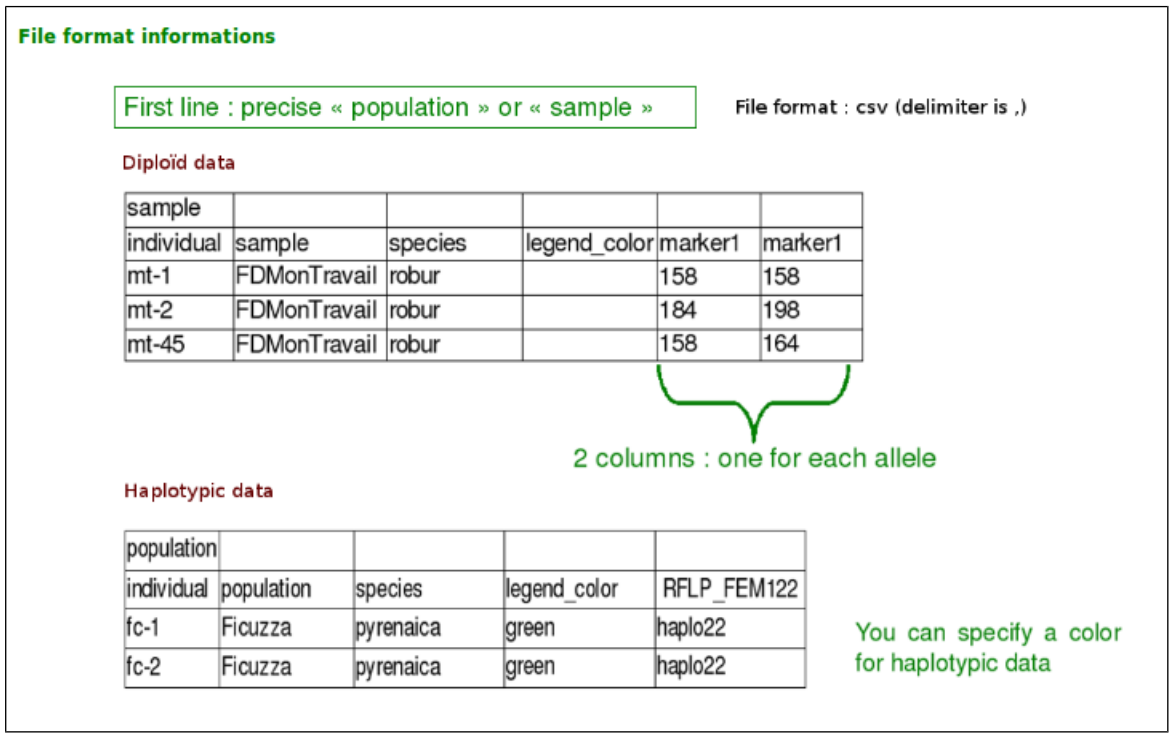
(a) Genotyping data

The importation is made from a csv file. Click on “Insert genotyping data”, then choose a project and a dataset to insert the data.



NB : The data inserted in a dataset belonging to the project Evoltree, will be visible from the eLab Wizard (Evoltree portal)

The csv file format is described below:


File format informations
First line : precise « population » or « sample »
File format : csv (delimiter is ,)
Diploïd data
sample
individual sample species legend_color marker1 marker1
mt-1 FDMonTravail robur 158 158
mt-2 FDMonTravail robur 184 198
mt-45 FDMonTravail robur 158 164
2 columns : one for each allele
Haplotypic data
population
individual population species legend_color RFLP_FEM122
fc-1 Ficuzza pyrenaica green haplo22
fc-2 Ficuzza pyrenaica green haplo22
You can specify a color for haplotypic data

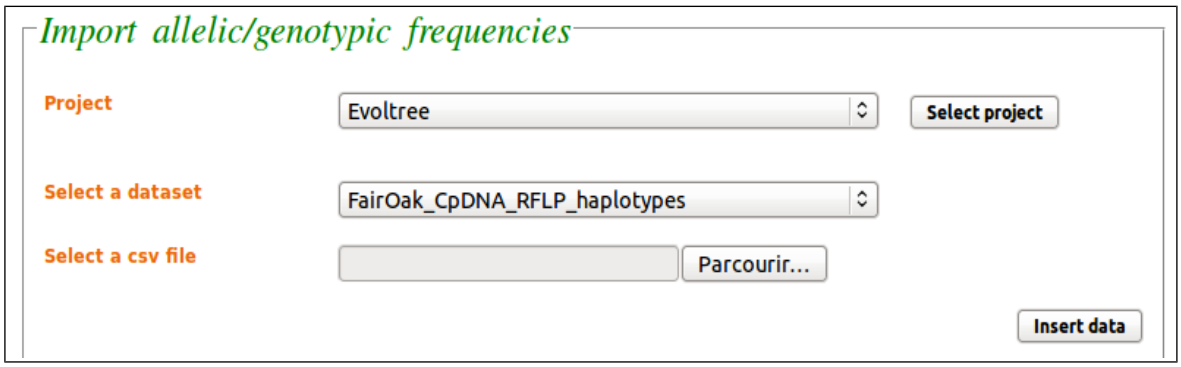
For the haplotypes, it's possible to define the color that will be used for the pie charts for the display of haplotypic frequencies in the column “legend_color”.

(b) Diversity data

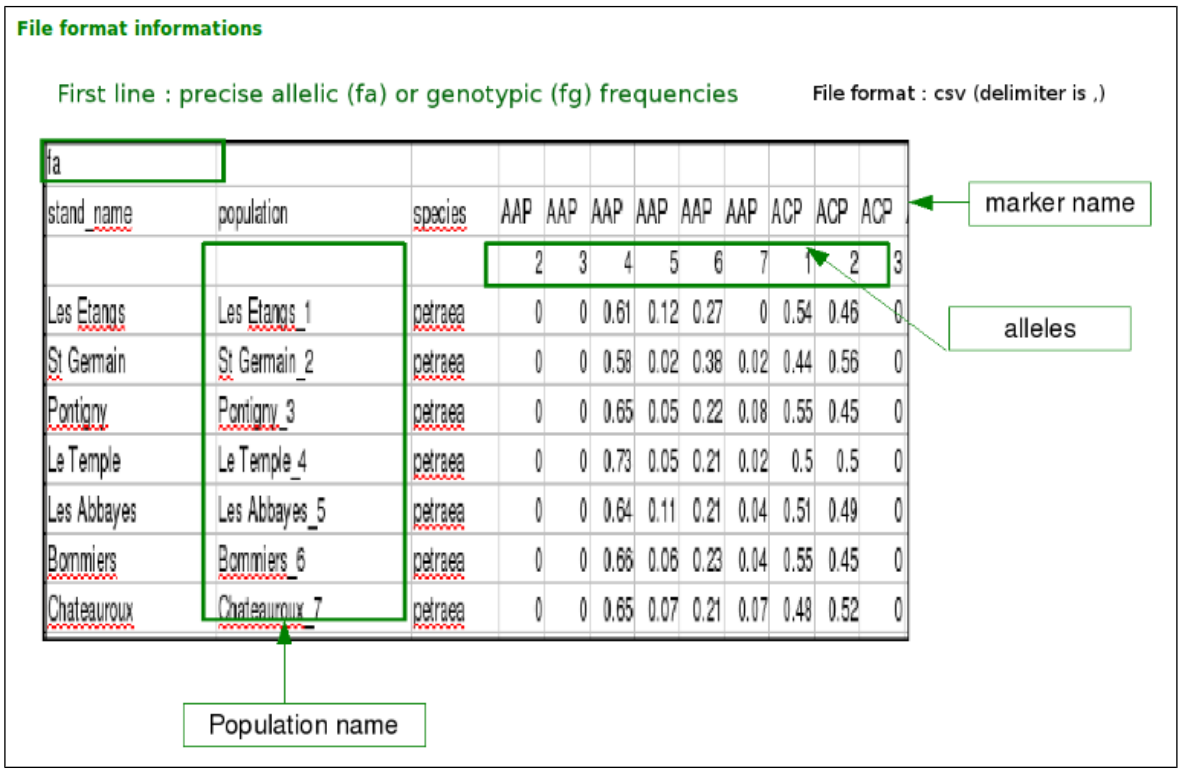
It involves data collected on the population level comprise frequencies and diversity statistics (diversity indices, allelic and haplotypic frequencies, ...)

- Insert Allelic/Genotypic frequencies

To access to it : *Add Genetic Data* > *Insert Diversity data* > *Insert Allelic/Genotypic Frequencies*. Then select a project and a dataset.



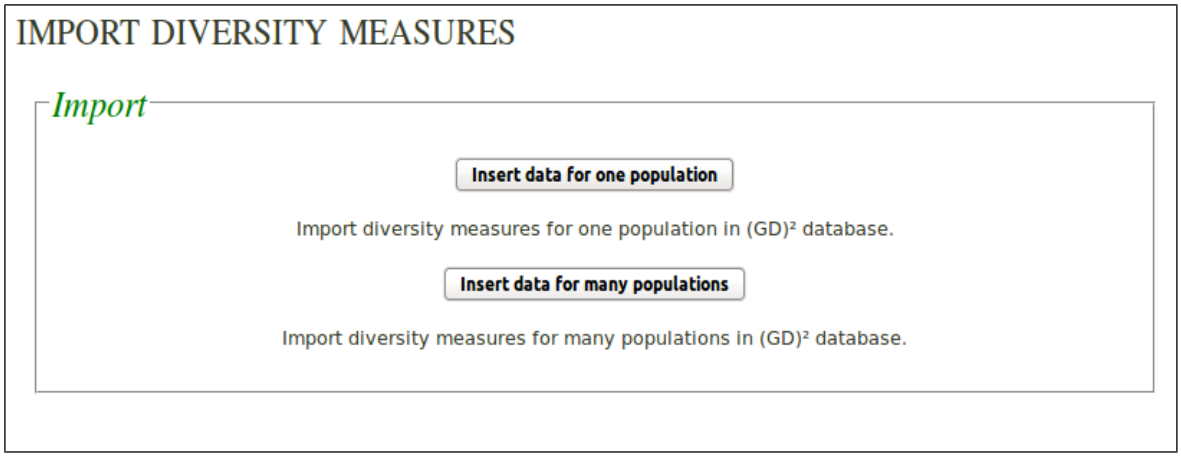
The csv file format is explained below.



The mentioned markers and populations in the file must exist in the database. So please, **check their spelling**.
The marker names in the second line and population names in the second column should be the same than those already introduced during the previous steps, when the population and marker data were introduced. So please, **check their spelling**.

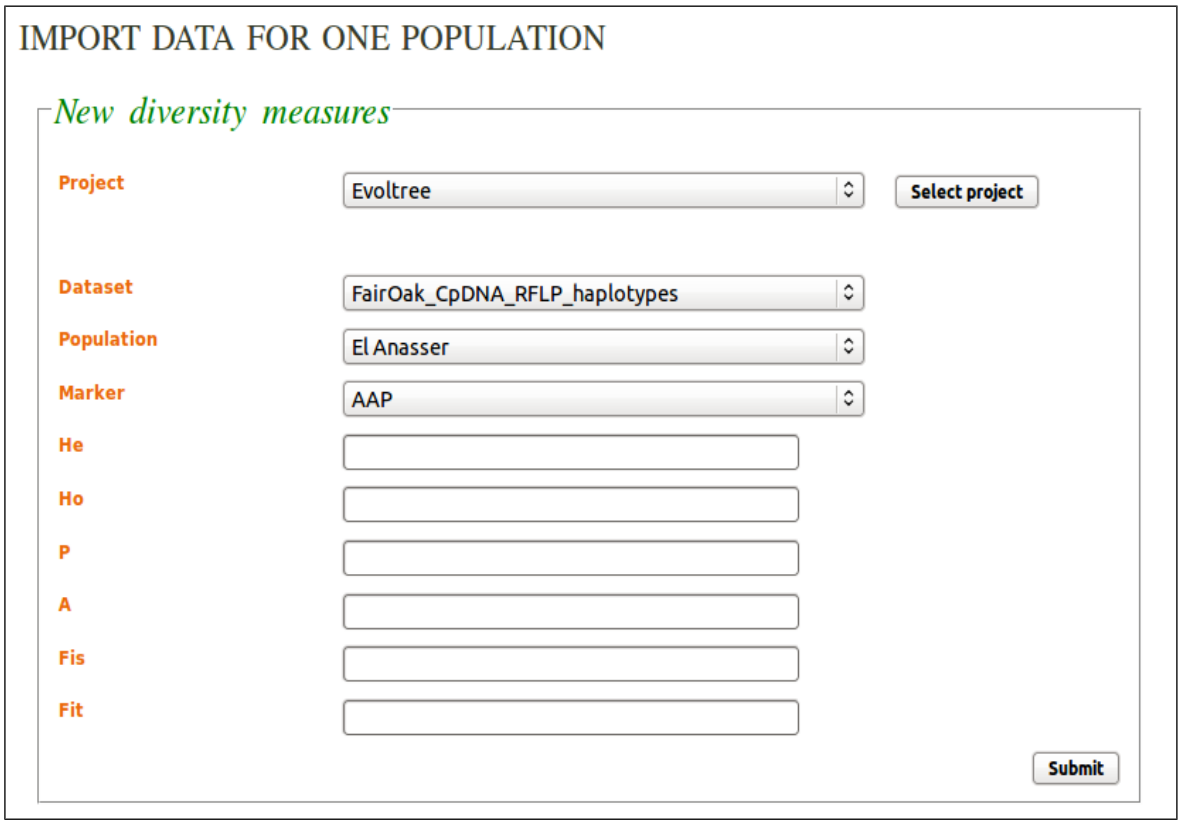
- Insert values for diversity index

Diversity indices refer either to a given marker or a set of markers used in a study (all used markers in a dataset) . To access to this insertion : *Add Genetic Data > Insert Diversity Data.* You can insert data for one population or for many populations in (GD)² database.


IMPORT DIVERSITY MEASURES
Import
Insert data for one population
Import diversity measures for one population in (GD)² database.
Insert data for many populations
Import diversity measures for many populations in (GD)² database.

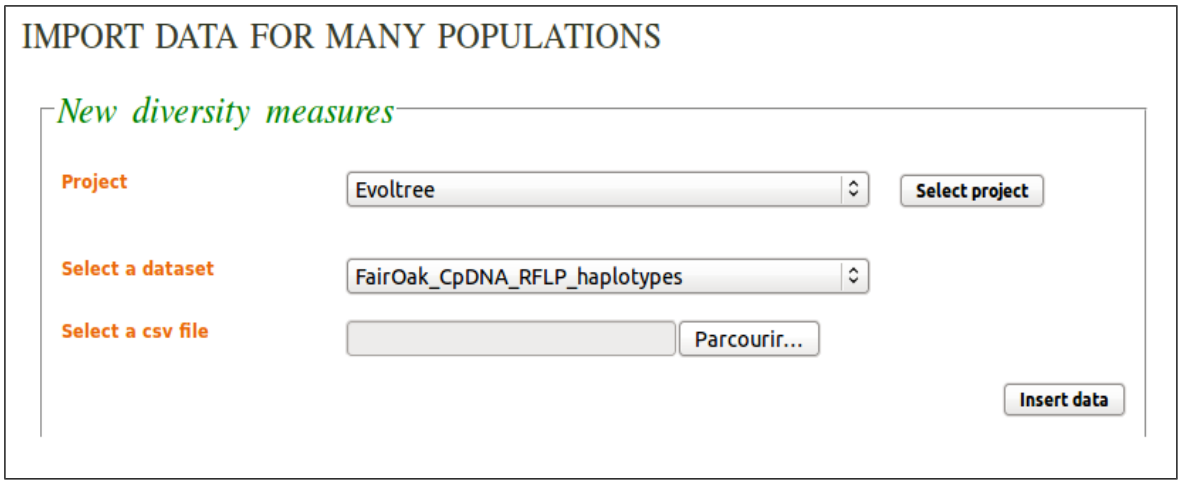
- Insert data for one population

This menu allows to import diversity measures for one population in (GD)² database. Click on your project, choose a dataset, a population, a marker and seize values for indices (He, Ho, P, A, Fis, Fit).



- Insert data for many populations

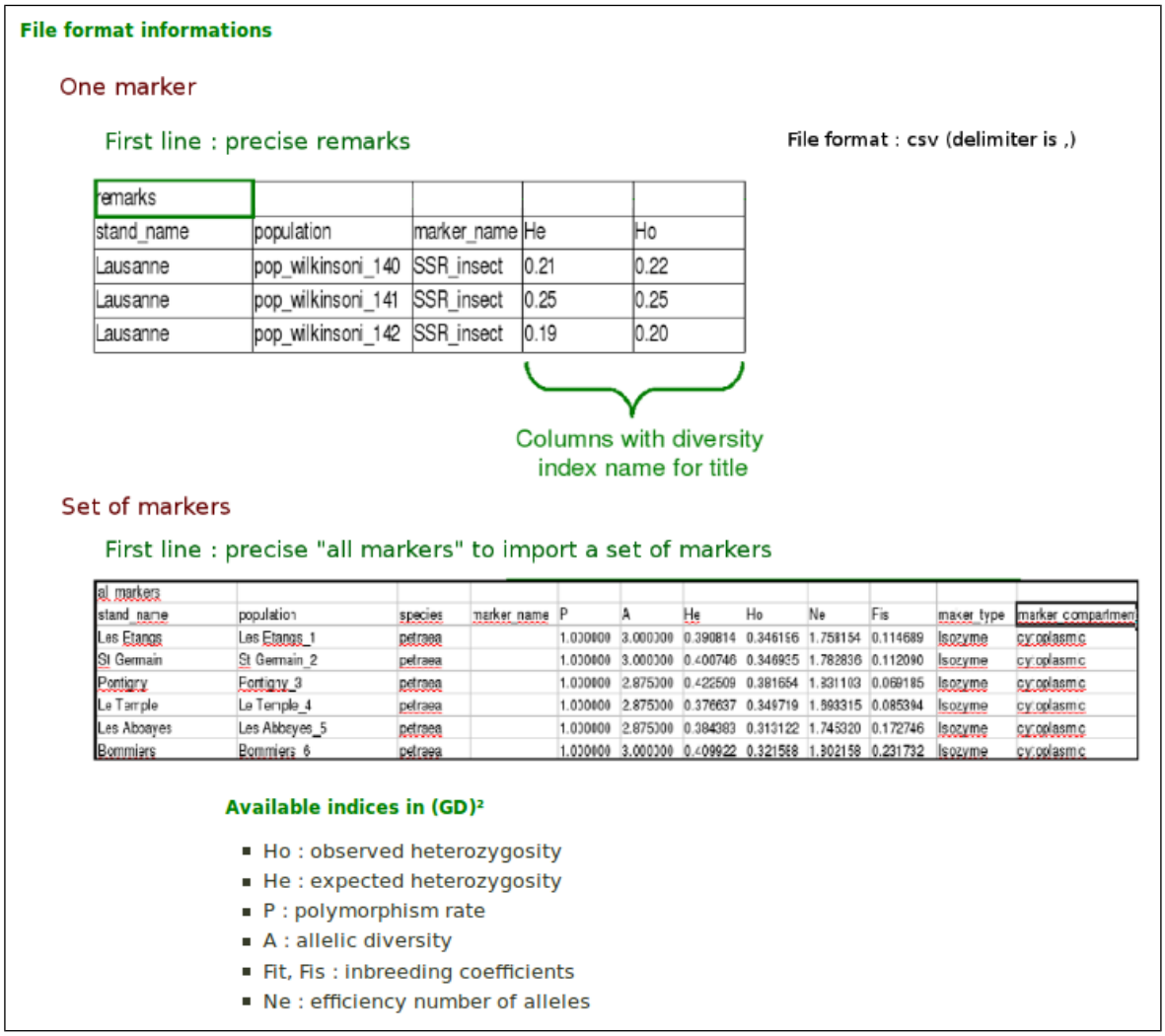
This menu allows to import diversity measures for many populations in (GD)² database. Click on your project, choose a dataset and select your csv file containing data.



Available indices in (GD)² are the following :

- Ho : observed heterozygosity
- He : expected heterozygosity
- P : polymorphism rate
- A : allelic diversity
- Fit, Fis : inbreeding coefficients
- Ne : efficiency number of alleles

The csv file format is explained below.



File format informations

One marker

First line : precise remarks

File format : csv (delimiter is ,)

remarks				
stand_name	population	marker_name	He	Ho
Lausanne	pop_wilkinsoni_140	SSR_insect	0.21	0.22
Lausanne	pop_wilkinsoni_141	SSR_insect	0.25	0.25
Lausanne	pop_wilkinsoni_142	SSR_insect	0.19	0.20

Columns with diversity index name for title

Set of markers

First line : precise "all markers" to import a set of markers

al_markers											
stand_name	population	species	marker_name	P	A	He	Ho	Ne	Fis	marker_type	marker_compartmen
Les Etangs	Les Etangs_1	petraea		1.000000	3.000000	0.390814	0.346156	1.758154	0.114689	Isozyme	cytoplasmic
St Germain	St Germain_2	petraea		1.000000	3.000000	0.400746	0.346935	1.782836	0.112090	Isozyme	cytoplasmic
Pontigny	Pontigny_3	petraea		1.000000	2.875000	0.422509	0.381654	1.831103	0.069185	Isozyme	cytoplasmic
Le Temple	Le Temple_4	petraea		1.000000	2.875000	0.376637	0.349719	1.993315	0.085394	Isozyme	cytoplasmic
Les Abbayes	Les Abbayes_5	petraea		1.000000	2.875000	0.384383	0.313122	1.745320	0.172746	Isozyme	cytoplasmic
Bommiers	Bommiers_6	petraea		1.000000	3.000000	0.409922	0.321568	1.902158	0.231732	Isozyme	cytoplasmic

Available indices in (GD)²

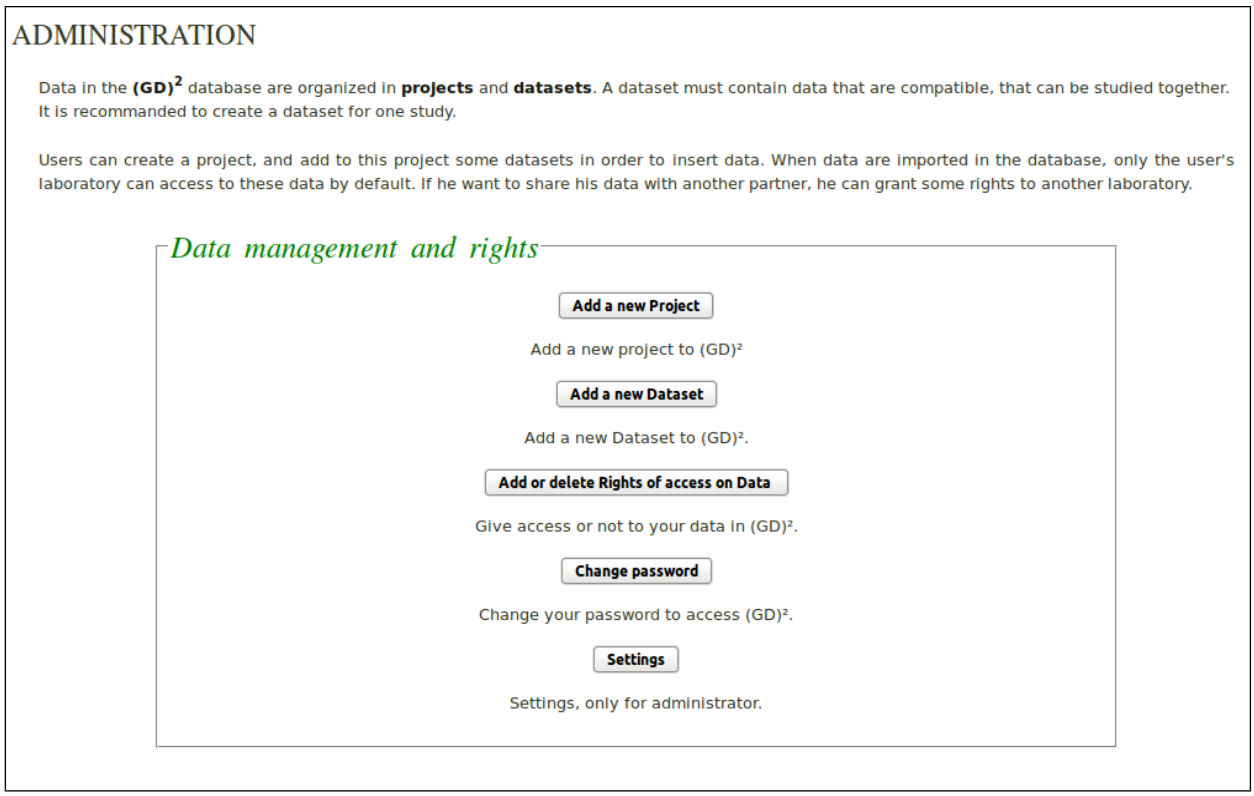
- Ho : observed heterozygosity
- He : expected heterozygosity
- P : polymorphism rate
- A : allelic diversity
- Fit, Fis : inbreeding coefficients
- Ne : efficiency number of alleles

III. Administration

The administration part of the web application is reachable from the menu.

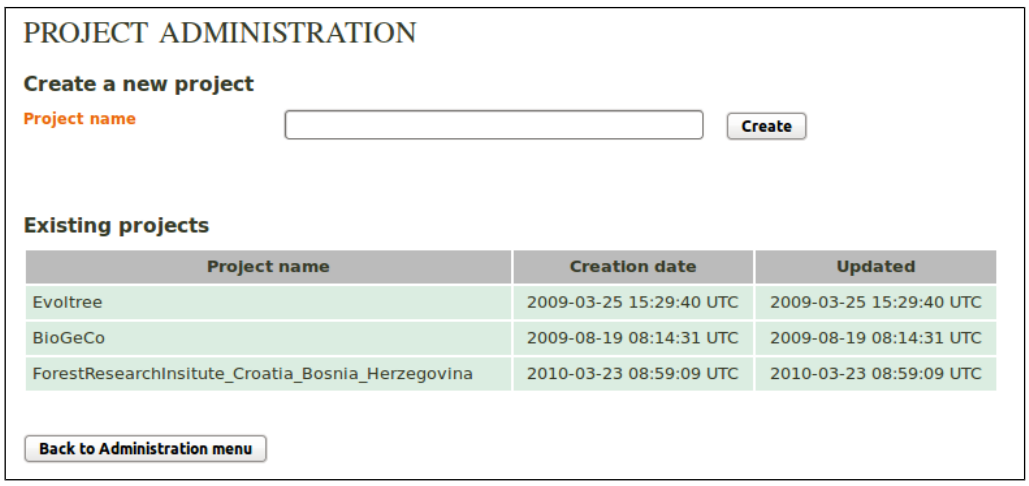
Data in the **(GD)^2** database are organized in **projects** and **datasets**. A dataset must contain data that are compatible, that can be studied together. It is recommanded to create a dataset for one study (example : all data that are involved in a publication subject). A dataset belongs to a project.

Users can create a project, and add to this project some datasets in order to insert data. When data are imported in the database, only the user's laboratory can access to these data by default. If he want to share his data with another partner, he can grant some rights to another laboratory.


ADMINISTRATION
Data in the (GD)2 database are organized in projects and datasets. A dataset must contain data that are compatible, that can be studied together. It is recommanded to create a dataset for one study.
Users can create a project, and add to this project some datasets in order to insert data. When data are imported in the database, only the user's laboratory can access to these data by default. If he want to share his data with another partner, he can grant some rights to another laboratory.
Data management and rights
Add a new Project
Add a new project to (GD)²
Add a new Dataset
Add a new Dataset to (GD)².
Add or delete Rights of access on Data
Give access or not to your data in (GD)².
Change password
Change your password to access (GD)².
Settings
Settings, only for administrator.

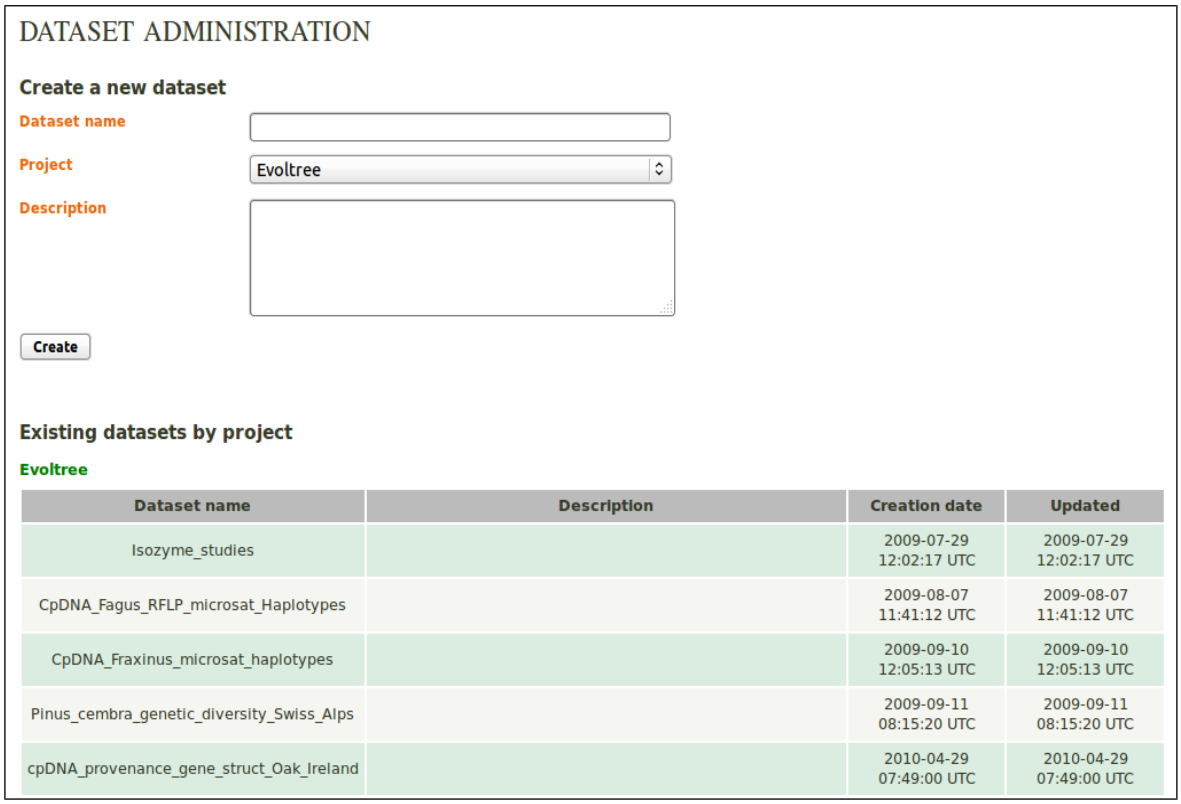
1. Add a new Project

To create a new project, click on the “Add a new Project” button. A simple form allows to create a new project and to view existing projects in the database.



2. Add a new dataset

To create a new dataset, click on the “Add a new Dataset” button. A simple form allows to create a new dataset and to view existing datasets, by project, in the database.



NB : all tied datasets (that involves all included data) to the Evoltree project, will be visible from the eLab Search Wizard of the official portal of the Network of Excellence Evoltree (http://www.evoltree.eu).

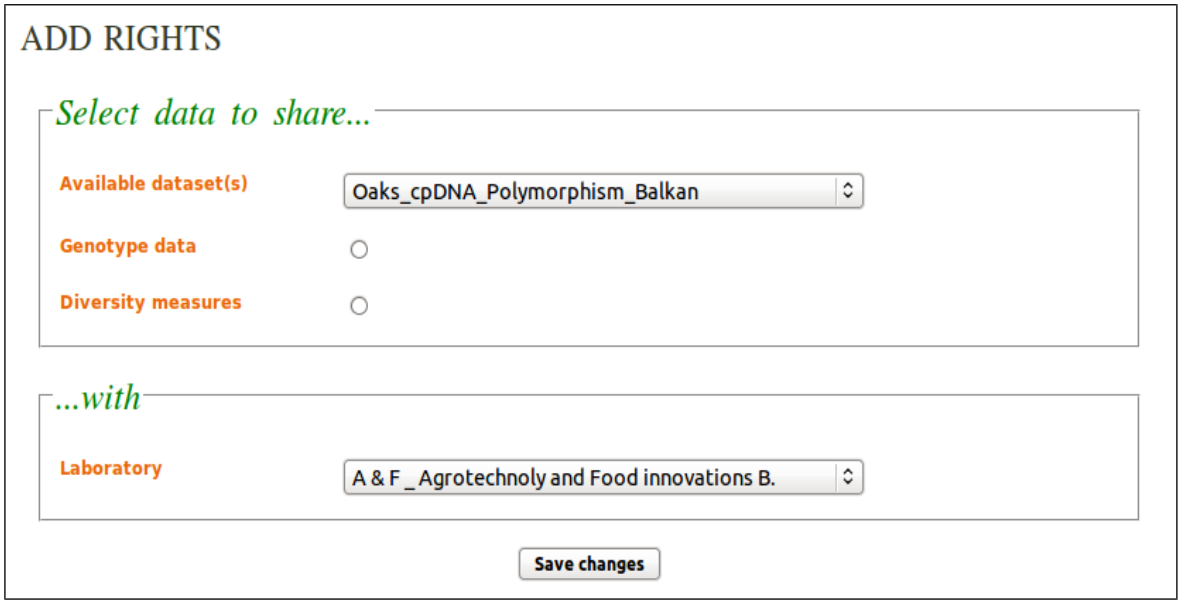
3. Add or delete rights of access on data

When a user import his data in the database, only his laboratory can access to these data. If he want to share his data with another partner, he can grant some rights to another laboratory. To access to this function : *Administration* > *Add or delete rights of access on Data*.

Add/Modify Rights
Add rights
If you want to share data with another partner or laboratory.
Delete rights
If you want to delete rights on data.

1) Add rights

When you click on “Add rights”, we access to a form.



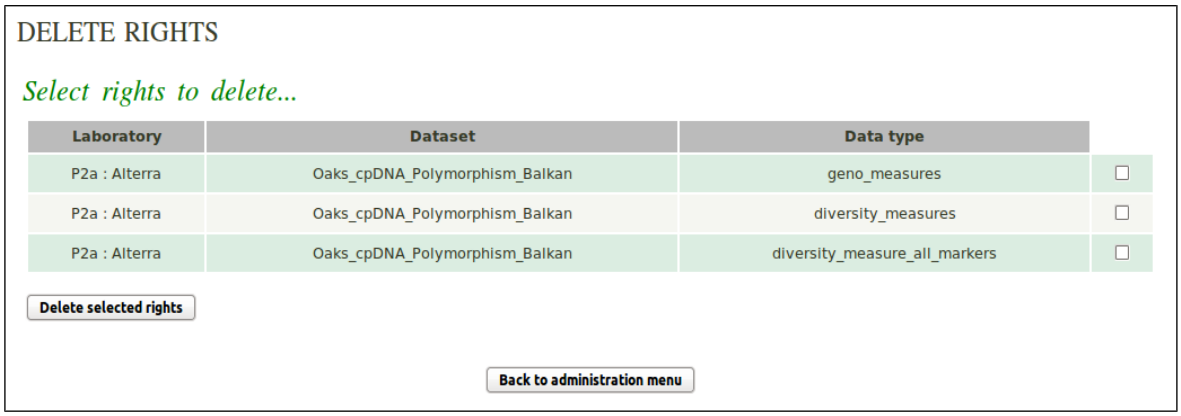
Then you can select :

- the dataset
- the data type (genotyping or diversity)
- the partner laboratory

These informations are validated by clicking on “Save changes”. The chosen partner laboratory can access to the data from the viewer.

2) Delete rights

To delete rights on data, click on “Delete rights”. A list displays all laboratories for which you have granted some rights, according to dataset and data type.



We check in this list the rights to delete then we validate by clicking on “Delete selected rights”. This deletion takes effect immediately.

3) Change password

To change your password, click on “Change password”. All informations about your account are displayed (last name, first name, e-mail, etc...). Type, re-type your new password and click on the “Save changes” button. This modification takes effect immediately. Logout, and then login with your new password.

IV. Acknowledgements

For remarks or any suggestions, thanks to get in touch with Audrey Jacques-Gustave (audrey@pierroton.inra.fr) or Frederic Raspail (Frederic.Raspail@pierroton.inra.fr).